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OM nucleic - nucleic search, using sw model

Run on: November 12, 2003, 22:40:30 ; Search time 9691 Seconds
(without alignments)
11503.326 Million cell updates/sec

Title: US-10-054-678-1
Perfect score: 2725
Sequence: 1 tcagtcgctgggccagcctg.....aagctcacacttgggctggc 2725

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2725	100.0	2725	6	AX356102	AX356102 Sequence
2	2725	100.0	2725	9	HSDBHRA	X13255 Human mRNA
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4	2425	89.0	2425	9	HSDBHRB	X13256 Human mRNA
5	1940	71.2	1955	9	HSDBH	Y00096 Human mRNA
6	1805.2	66.2	1812	12	BT007470	BT007470 Synthetic
7	1702.8	62.5	3842	4	AB029430	AB029430 Equus cab
8	1498	55.0	2317	4	AF118638	AF118638 Bos tauru
9	1476.8	54.2	2322	4	BOVADBM	J02890 Bovine adre
10	1419.2	52.1	1840	4	BOVDBH	J05160 Bovine dopa
11	1412.8	51.8	2195	4	BOVDBHZ	J02909 Bovine dopa
12	1236.8	45.4	2274	10	S50200	S50200 Mus musculu
13	1219.4	44.7	2443	10	RATDOPBHY	L12407 Rattus norv
14	1016.8	37.3	1092	9	HSDBH12	X13268 Human DNA f
c 15	1016.8	37.3	46651	9	AC000404	AC000404 Genomic s
16	1016.8	37.3	53242	9	AL365494	AL365494 Human DNA
c 17	1016.8	37.3	110000	2	AL954350_3	Continuation (4 of
18	1001.2	36.7	110000	2	AL954350_0	AL954350 Homo sapi
19	330	12.1	2037	9	HSDBH1	X13257 Human DNA f
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21	326.6	12.0	509	5	GGA251457	AJ251457 Gallus ga
22	258.4	9.5	276	9	HSDBH3	X13259 Human DNA f
23	239.6	8.8	262	9	AF070919	AF070919 Macaca mu
24	228.4	8.4	2894	3	DMTBHMR	Z70316 D.melanogas
25	228.4	8.4	73066	10	AL954801	AL954801 Mouse DNA
26	228.4	8.4	186208	2	AC010965	AC010965 Mus muscu
c 27	228.4	8.4	205420	2	AC091762	AC091762 Mus muscu
28	221.6	8.1	663	5	AF075385	AF075385 Danio rer
29	220	8.1	225079	2	AC126203	AC126203 Rattus no
c 30	193	7.1	2037	6	AX347199	AX347199 Sequence
c 31	193	7.1	2037	6	AX348532	AX348532 Sequence
32	180	6.6	195	9	HSDBH4	X13260 Human DNA f
33	179.6	6.6	2037	6	AX347198	AX347198 Sequence
34	179.6	6.6	2037	6	AX348531	AX348531 Sequence
35	175.8	6.5	2164	10	BC037684	BC037684 Mus muscu
36	174.2	6.4	2903	10	AB041606	AB041606 Mus muscu
37	172	6.3	2796	10	BC025892	BC025892 Mus muscu
38	170	6.2	185	9	HSDBH6	X13262 Human DNA f
c 39	166.8	6.1	2906	9	AF129263	AF129263 Homo sapi
40	163.8	6.0	178	9	HSDBH11	X13267 Human DNA f
41	151.4	5.6	2188	9	BC018756	BC018756 Homo sapi
42	149.2	5.5	162	9	HSDBH7	X13263 Human DNA f
43	149	5.5	165	9	HSDBH2	X13258 Human DNA f
44	146.8	5.4	2150	6	AX464056	AX464056 Sequence
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47	141.8	5.2	2762	9	AK074879	AK074879 Homo sapi
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52	131	4.8	146	9	HSDBH10	X13266 Human DNA f
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c 54	113	4.1	181178	3	AC023713	AC023713 Drosophil
55	113	4.1	315362	3	AE003442	AE003442 Drosophil
56	106	3.9	121	9	HSDBH5	X13261 Human DNA f
c 57	105	3.9	2139	9	AF129264	AF129264 Homo sapi
58	101.8	3.7	1860	10	AB065134	AB065134 Mus muscu
59	101	3.7	129616	2	AL935290	AL935290 Danio rer
60	94.6	3.5	155030	2	AC141807	AC141807 Apis mell
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62	88.8	3.3	2122	9	HSM800558	AL080058 Homo sapi
63	77.2	2.8	125020	9	AF429315	AF429315 Homo sapi
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65	65.8	2.4	2726	3	AY071594	AY071594 Drosophil

	66	65.8	2.4	59865	2	AC014422 AC014422 Drosophil
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	69	62.6	2.3	78	9	HSDBH9 X14357 Human DNA f
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	77	54	2.0	1572	1	BPEFLAGEL L13034 Bordetella
	78	53.8	2.0	295150	1	SCO939125 AL939125 Streptomy
	79	52.4	1.9	3739	1	MLUVRA X15867 Micrococcus
c	80	51.2	1.9	67480	7	AY129334 AY129334 Mycobacte
	81	50.8	1.9	1045	1	AF232940 AF232940 Bordetell
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	83	50	1.8	1396	6	AX527902 AX527902 Sequence
	84	50	1.8	1424	6	AX527904 AX527904 Sequence
	85	49.8	1.8	1512	6	AX077613 AX077613 Sequence
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	89	49.4	1.8	816	8	RICGA3 D83527 Rice (YK426
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	111	46.4	1.7	296500	1	SCO939128 AL939128 Streptomy
	112	46.2	1.7	1014	6	BD179703 BD179703 Highly th
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	114	46.2	1.7	1743	6	BD179535 BD179535 Highly th
	115	46.2	1.7	2636	9	HUMCOL6A2B M81835 Human alpha
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c	117	46.2	1.7	110000	2	LMFLCHR34_11 Continuation (12 o
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c	119	46	1.7	85758	9	AC068645 AC068645 Homo sapi
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ALIGNMENTS

RESULT 1
AX356102
LOCUS AX356102 2725 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0186000.
ACCESSION AX356102
VERSION AX356102.1 GI:18620653
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sklar,P., Lander,E.S., Mcinnis,M.G., Depaulo,J.R., Willour,V. and
Potash,J.
TITLE Association of dopamine beta-hydroxylase polymorphisms with bipolar disorder
JOURNAL Patent: WO 0186000-A 1 15-NOV-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE GENERAL HOSPITAL CORPORATION (US) ; JOHNS HOPKINS UNIVERSITY (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 533 a 901 c 774 g 517 t
ORIGIN

Query Match 100.0%; Score 2725; DB 6; Length 2725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
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Qy       2161 TCCGCCTCACTGGGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGG 2220
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Db       2161 TCCGCCTCACTGGGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGG 2220

Qy       2221 AATCACCGGGAACGCCCCCGCCCCCGCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AATCACCGGGAACGCCCCCGCCCCCGCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTG 2280

Qy       2281 CCGCTTAAACATTTCCCTGCTGAGTGGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGAC 2340
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Db       2281 CCGCTTAAACATTTCCCTGCTGAGTGGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGAC 2340

Qy       2341 GGAGGCAGGACCAGGCATTTAGCTAGTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTG 2400
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Db       2341 GGAGGCAGGACCAGGCATTTAGCTAGTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTG 2400

Qy       2401 AGTAAACAGATATTTTCGCCCACCTAAAGGGAAGCCCTGACAACAACTATCACCAAAAGA 2460
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Db       2401 AGTAAACAGATATTTTCGCCCACCTAAAGGGAAGCCCTGACAACAACTATCACCAAAAGA 2460

Qy       2461 CGAGGCGGCAAAGATCCAGCGGGGCTTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATT 2520
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Qy       2581 GCTGTGCTTTCCGCGTGGTTCTGCCACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACA 2640
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Qy       2641 TTCCTGACCCTCACTTTTCTCATCTGTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGC 2700
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RESULT 2
HSDBHRA
LOCUS HSDBHRA 2725 bp mRNA linear PRI 31-MAR-1995
DEFINITION Human mRNA for dopamine beta-hydroxylase type a (EC 1.14.17.1).
ACCESSION X13255
VERSION X13255.1 GI:30473
KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2725)
AUTHORS Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation

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  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 2725)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     see also X13256 for type b mRNA
            Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
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                     /note="signal peptide (AA -25 to -1)"
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                     /product="dopamine beta-hydroxylase (AA 1 - 578)"
BASE COUNT      533 a    901 c    774 g    517 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2725;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240
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Db        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
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Qy        301 GGACCGATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGACCGATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCC 360

Qy        361 ACCTGGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGA 420
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Db        361 ACCTGGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGA 420

Qy        421 CCCTGCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACG 480
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Qy        541 ACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCG 600
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Db        541 ACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCG 600

Qy        601 AACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCC 660

Qy        661 CCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 720
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Db        661 CCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 720

Qy        721 ACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACA 780
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Qy        781 TGGAAGTCTTCCAGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCG 840
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Db        781 TGGAAGTCTTCCAGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCG 840

Qy        841 ACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCC 900
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Qy        901 TGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGT 960
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Db        901 TGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGT 960

Qy        961 CCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAA 1020
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Qy       1021 ACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGA 1080

Qy       1081 TCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCT 1140
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Db       1081 TCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCT 1140

Qy       1141 TCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGA 1200
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Qy       1201 TCCACATCTTCGCCTCTCAGCTCCACACACACCTGACTGGGAGAAAGGTGGTCACAGTGC 1260
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Qy       1321 TCCAGGAGATCCGCATGTTGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCA 1380
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Qy      1861 CCCCCTCCTCCATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTGCGAC 1920
Db      1861 CCCCCTCCTCCATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTGCGAC 1920
Qy      1921 GATCCCCATGGAACAGCCCTGCACGCCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTG 1980
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RESULT 3
BC017174

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LOCUS       BC017174                2807 bp    mRNA    linear   PRI 09-NOV-2001
DEFINITION  Homo sapiens, dopamine beta-hydroxylase (dopamine
            beta-monooxygenase), clone MGC:2350 IMAGE:3163986, mRNA, complete
            cds.
ACCESSION   BC017174
VERSION     BC017174.1  GI:16877892
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2807)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site:       http://www.nisc.nih.gov/
            Contact:        nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 5 Row: g Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4503260.
FEATURES             Location/Qualifiers
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                     /note="Vector: pOTB7"
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                     NNEDVCTCPQASVSQQFTSVPWNSFNRDVLKALYSFAPISMHCNKSSAVRFQGEWNLQ
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BASE COUNT      589 a    909 c    788 g    521 t
ORIGIN

  Query Match           99.7%;  Score 2717;  DB 9;  Length 2807;
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  Matches 2720;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
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Db         15 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 74

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Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
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Qy        301 GGACCGATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCC 360
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Qy        361 ACCTGGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGA 420
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Qy        421 CCCTGCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACG 480
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Qy        481 GCACTGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCA 540
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Qy        541 ACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCG 600
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Qy        661 CCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 720
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Qy        721 ACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACA 780
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Qy        841 ACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCC 900
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Qy        961 CCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAA 1020
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RESULT 4
HSDBHRB
LOCUS       HSDBHRB                 2425 bp    mRNA    linear   PRI 31-MAR-1995
DEFINITION  Human mRNA for dopamine beta-hydroxylase type b (EC 1.14.17.1).
ACCESSION   X13256
VERSION     X13256.1  GI:30477
KEYWORDS    alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2425)
  AUTHORS   Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
  TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
            different 3'-terminal regions are produced through alternative
            polyadenylation
  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 2425)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
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ORIGIN
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  Matches 2425;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       2101 TGACTCAGTGCAGGGACAGCCCGCACAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGT 2160
Qy       2161 TCCGCCTCACTGGGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGG 2220
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Qy       2221 AATCACCGGGAACGCCCCCGCCCCCGCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTG 2280
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Qy       2281 CCGCTTAAACATTTCCCTGCTGAGTGGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGAC 2340
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Qy       2341 GGAGGCAGGACCAGGCATTTAGCTAGTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTG 2400
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Qy       2401 AGTAAACAGATATTTTCGCCCACCT 2425
Db       2401 AGTAAACAGATATTTTCGCCCACCT 2425
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RESULT 5
HSDBH
LOCUS       HSDBH                   1955 bp    mRNA    linear   PRI 31-MAR-1995
DEFINITION  Human mRNA for dopamine beta-hydroxylase (EC 1.14.17.1).
ACCESSION   Y00096
VERSION     Y00096.1  GI:30455
KEYWORDS    dopamine beta-hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 1955)
  AUTHORS   Lamouroux,A., Vigny,A., Faucon Biguet,N., Darmon,M.C., Franck,R.,
            Henry,J.P. and Mallet,J.
  TITLE     The primary structure of human dopamine-ss-hydroxylase: insights
            into the relationship between the soluble and the membrane-bound
            forms of the enzyme
  JOURNAL   EMBO J. 6, 3921-3937 (1987)
FEATURES             Location/Qualifiers
     source          1. .1955
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BASE COUNT      394 a    665 c    538 g    358 t
ORIGIN

  Query Match             71.2%;  Score 1940;  DB 9;  Length 1955;
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  Matches 1943;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 67

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
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Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
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Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
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Qy        361 ACCTGGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGA 420
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Db        428 CCCTGCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAGGACG 487

Qy        481 GCACTGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCA 540
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Qy        541 ACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCG 600
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Qy        601 AACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCC 660
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Db        608 AACCGGAGTTGCCCTCAGACACGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCC 667

Qy        661 CCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 720
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Db        668 CCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC 727

Qy        721 ACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACA 780
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Qy        781 TGGAAGTCTTCCAGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCG 840
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Qy        841 ACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCC 900
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Qy        961 CCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAA 1020
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Qy       1081 TCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCT 1140
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Db       1088 TCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCT 1147

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Qy       1381 CCTCCTGCACGTACAACACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGGGATCC 1440
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Qy       1861 CCCCCTCCTCCATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTGCGAC 1920
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Qy       1921 GATCCCCATGGAACAGCCCTGCACGCCC 1948
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RESULT 6
BT007470
LOCUS BT007470 1812 bp mRNA linear SYN 13-MAY-2003
DEFINITION Synthetic construct Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) mRNA, partial cds.
ACCESSION BT007470
VERSION BT007470.1 GI:30583778
KEYWORDS FLI_CDNA.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1812)
AUTHORS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1812)
AUTHORS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
FEATURES Location/Qualifiers
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BASE COUNT 372 a 600 c 505 g 335 t
ORIGIN

Query Match 66.2%; Score 1805.2; DB 12; Length 1812;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1807; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db          1 ATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATCTTCCTGGTCATCCTGGTG 60

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Qy        273 CTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGACACTGCCTATTTTGCGGAC 332
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Db        301 GCCTGGAGTGACCAGAAGGGGCAGATCCACCTGGATCCCCAGCAGGACTACCAGCTGCTG 360

Qy        393 CAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGCCCTTTGGCACCTGC 452
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Db        361 CAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGCCCTTTGGCACCTGC 420

Qy        453 GACCCCAAGGATTACCTCATTGAAGACGGCACTGTCCACTTGGTCTACGGGATCCTGGAG 512
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Db        421 GACCCCAAGGATTACCTCATTGAGGACGGCACTGTCCACTTGGTCTACGGGATCCTGGAG 480

Qy        513 GAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCCTGCAGATGGGGCTGCAGAGG 572
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Qy        933 GCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTCCGCCTGGAAGTTCACTAC 992
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Qy        993 CACAACCCACTGGTGATAGAAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACA 1052
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Db       1201 CTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTG 1260

Qy       1293 AACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTCGTG 1352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTCGTG 1320

Qy       1353 TCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACACGGAAGACCGGGAG 1412
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Db       1321 TCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACACGGAAGACCGGGAG 1380

Qy       1413 CTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCAACTACGTGCACTAC 1472
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Db       1381 CTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCAACTACGTGCACTAC 1440

Qy       1473 TACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGCTTCCTGCAGAAG 1532
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db       1441 TACCCCCAGACGCAGCTGGAGCTCTGCAAGAGCGCTGTGGACGCCGGCTTCCTGCAGAAG 1500

Qy       1533 TACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTCTGCACCTGCCCTCAGGCGTCC 1592
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Qy       1593 GTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAACCGCGACGTACTGAAGGCC 1652
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Db       1561 GTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAACCGCGACGTACTGAAGGCC 1620

Qy       1653 CTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCCTCAGCCGTCCGCTTCCAG 1712
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Db       1621 CTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCCTCAGCCGTCCGCTTCCAG 1680

Qy       1713 GGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCCCACCCCA 1772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCCCACCCCA 1740

Qy       1773 CAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCATTGGTGGG 1832
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Db       1741 CAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCATTGGTGGG 1800

Qy       1833 GGCAAAGGCT 1842
              ||||||||||
Db       1801 GGCAAAGGCT 1810


RESULT 7
AB029430
LOCUS       AB029430               3842 bp    mRNA    linear   MAM 06-JUL-1999
DEFINITION  Equus caballus DBH mRNA for dopamine beta-hydroxylase, complete
            cds.
ACCESSION   AB029430
VERSION     AB029430.1  GI:5381206
KEYWORDS    dopamine beta-hydroxylase.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 3842)
  AUTHORS   Sato,F., Ishida,N. and Hasegawa,T.
  TITLE     Equine dopamine beta-hydroxylase (DBH) mRNA, complete cds
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 3842)
  AUTHORS   Sato,F., Ishida,N. and Hasegawa,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-1999) Fumio Sato, Japan Racing Association Equine
            Research Institute, Laboratory of Molecular and Cellular Biology;
            321-4 Tokami-cho, Utsunomiya 320-0856, Japan
            (E-mail:fumios@center.equinst.go.jp, Tel:81-28-647-0662,
            Fax:81-28-647-0686)
FEATURES             Location/Qualifiers
     source          1. .3842
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                     PPSGIHIFASQLHTHLTGRKVVTVLARDGRREREVVNRDDHYSPHFQEIRMLKKVVSVH
                     PGDVLITSCTYNTEDRKLATVGGFGILEEMCVNYVHYYPQTQLELCKSAVDPGFLQKY
                     FHFVNRFNGEEVCTCPQASVPEQFATVPWNSFNRQVLSALYGFAPISMHCNRSSAVRF
                     QGDWNLQPLPEIISKLEEPTPRCPASRGRSPAGPTVVDIGGGKG"
BASE COUNT      725 a   1289 c   1085 g    743 t
ORIGIN

  Query Match           62.5%;  Score 1702.8;  DB 4;  Length 3842;
  Best Local Similarity   79.9%;  Pred. No. 9.1e-308;
  Matches 2177;  Conservative    0;  Mismatches  507;  Indels   40;  Gaps   13;

Qy         19 TGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATCTTCC 78
              | ||| |||||||| |||| |||||||| | ||||||| ||||||| ||||||||||||
Db         13 TCCCCAGCCCCAGCGTGCGCGAGGCAGCTTCCATGTACGGCACAGCGGTGGCCATCTTCC 72

Qy         79 TGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCCTATC 138
              |||||||||||||||||| |||||||||||||  ||||  ||||||||| | || || |
Db         73 TGGTCATCCTGGTGGCCGCGCTGCAGGGCTCGGAACCCCCCGAGAGCCCCTTTCCTTACC 132

Qy        139 ACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACCCAGG 198
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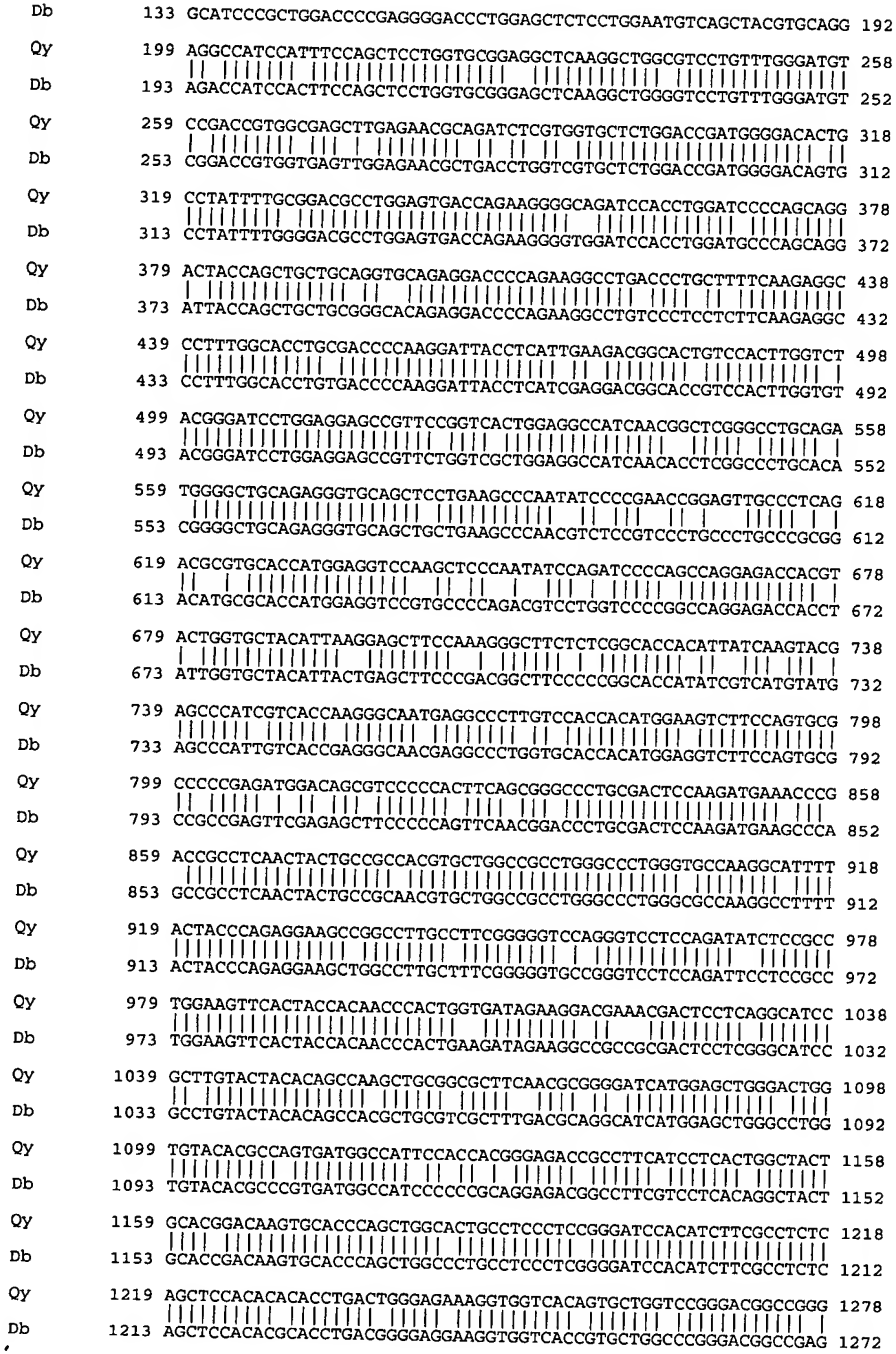

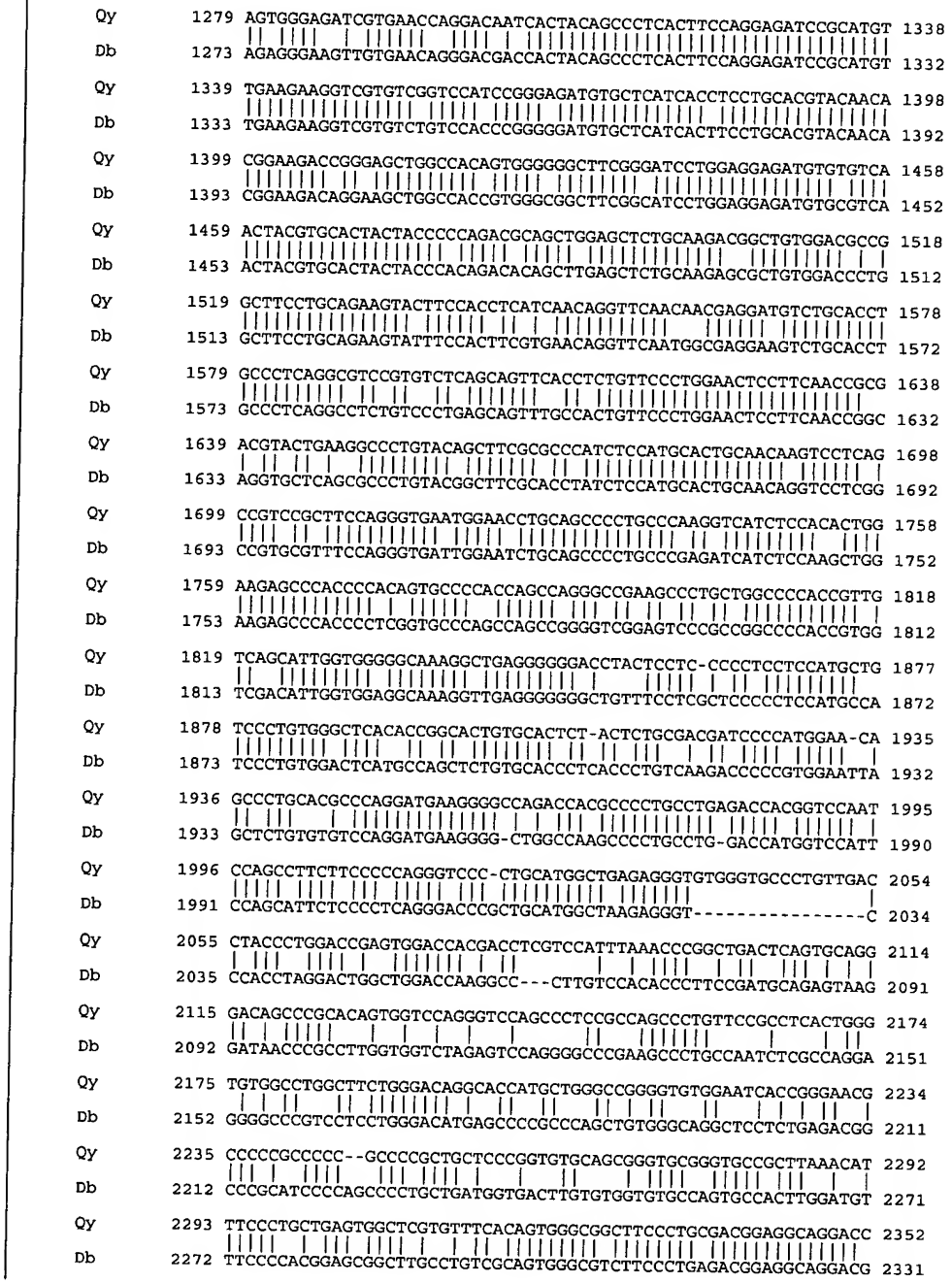

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Qy       2353 AGGCATTTAGCTAGTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATA 2412
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Db       2332 AGCCACTTAGCTAGTTAGAGACGTGCCTGGGAAATTGCTCCACTGCAGGGTAAATAGATA 2391

Qy       2413 TTTTCGCCCACCTAAAGGGAAGCCCTGACAACAACTATCACCA-----AAAGACGAGGCG 2467
             |||||||||||||||||| ||  ||| ||||||||  ||||||     |||||| || ||
Db       2392 TTTTCGCCCACCTAAAGGCAA-ACCTAACAACAACCCTCACCACCACCAAAGACAAGACG 2450

Qy       2468 GCAAAGATCCAGCGGGGCTTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCA 2527
             || |||||||||     |  || ||| ||| | |||  | |||   |       |    |||
Db       2451 GCGAAGATCCAGACAAGGATCCGGGTGCCAGCTCCTTGGGGGAATGGGGCGAT-TAGCCA 2509

Qy       2528 GCTTGCTTCTCTGCCGGTGGGGCCAGCGCTGAACAGACC------GGGGTGGAGTCAGGG 2581
             |  |||||||| |  |  ||  | | | ||||||||      |   ||| |||||
Db       2510 GGCTGCTTCTCTCCACGCTGGAACGGTGGTTAACAGACCATCTGGGCTCTGGGGTCAGAC 2569

Qy       2582 CTGTGCTTTCCGCGTGGTTCTGCCACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACAT 2641
             ||||      | ||      |  |      | ||||  || ||||||||||||||||  |
Db       2570 CTGTCAGAAGCCCGGTTCCATCTCTGGGGCTGGGTGTCACTCGGGCGGGCCATTTCACCT 2629

Qy       2642 TCCTGACCCTCACTTTTCTCATCTGTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCC 2701
             |||  |||||   |||||||||||||||||   |||  | || ||| ||| | |||||
Db       2630 CCCTCACCCTGGGTTTTCTCATCTGTAAAATGGGGCCAACGCTGTGTGGGTTGATGAGAT 2689

Qy       2702 AATAAAGCTCACACTTGGGCTGGC 2725
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Db       2690 GATAAAGTCCCCATGGGGGCCAGC 2713
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RESULT 8
AF118638
LOCUS       AF118638               2317 bp    mRNA    linear   MAM 26-JAN-1999
DEFINITION  Bos taurus dopamine beta-hydroxylase precursor (DBH) mRNA, complete
            cds.
ACCESSION   AF118638
VERSION     AF118638.1  GI:4191613
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 2317)
  AUTHORS   Wu,H.J., Parmer,R.J., Koop,A.H., Rozansky,D.J. and O'Connor,D.T.
  TITLE     Molecular cloning, structure, and expression of
            dopamine-beta-hydroxylase from bovine adrenal medulla
  JOURNAL   J. Neurochem. 55 (1), 97-105 (1990)
  MEDLINE   90285664
   PUBMED   1693949
REFERENCE   2  (bases 1 to 2317)
  AUTHORS   Wu,H.J., Parmer,R.J., Koop,A.H., Rozansky,D.J. and O'Connor,D.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-1999) Medicine (9111H), UCSD, 3350 La Jolla
            Village Drive, San Diego, CA 92161, USA
FEATURES             Location/Qualifiers
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                     /tissue_type="adrenal medulla"
     gene            1. .2317
                     /gene="DBH"
     CDS             38. .1831
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                     /product="dopamine beta-hydroxylase precursor"
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                     HVLAAWALGAKAFYYPEEAGLAFGGPGSSRFLRLEVHYHNPLVITGRRDSSGIRLYYT
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BASE COUNT      422 a    813 c    687 g    395 t
ORIGIN
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  Best Local Similarity   81.0%;  Pred. No. 1.7e-269;
  Matches 1825;  Conservative    0;  Mismatches  400;  Indels   27;  Gaps    6;

Qy         19 TGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATCTTCC 78
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Db          6 TCCCCAGCCCCAGCGTGCGCGAGGCGGCCTCCATGTACGGCACCGCGGTCGCCGTCTTCC 65

Qy         79 TGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCCTATC 138
              |||||||||| ||||| |||||||||||||||||| |||   |||||||| |||||  |
Db         66 TGGTCATCCTCGTGGCTGCACTGCAGGGCTCGGCCCCCGCCGAGAGCCCCTCCCCCTTCC 125

Qy        139 ACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACCCAGG 198
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Db        126 ACATCCCCCTGGACCCCGAGGGGACCCTGGAGCTGTCCTGGAACATCAGCTATGCGCAGG 185

Qy        199 AGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCCTGTTTGGGATGT 258
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Db        186 AGACCATCTACTTCCAGCTCCTGGTGCGGGAGCTCAAGGCTGGTGTCCTGTTTGGGATGT 245

Qy        259 CCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGACACTG 318
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Db        246 CGGACCGAGGGGAGCTGGAGAATGCTGACTTGGTGGTGCTCTGGACTGACAGGGACGGCG 305

Qy        319 CCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTGGATCCCCAGCAGG 378
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Db        306 CCGACTTTGGGGATGCCTGGAGTGACCAGAAGGGGCAGGTCCACCTGGACTCCCAGCAGG 365

Qy        379 ACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGC 438
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Db        366 ATTACCAGCTTCTGCGGGCACAGAGGACTCCAGAAGGCCTGTACCTGCTCTTCAAGAGGC 425

Qy        439 CCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACTGTCCACTTGGTCT 498
              | |||||||||| |||||||| || |||||||| || |||||||| |||||| |||| |
Db        426 CTTTTGGCACCTGTGACCCCAACGACTACCTCATCGAGGACGGCACCGTCCACCTGGTGT 485

Qy        499 ACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCCTGCAGA 558
              | ||  |||||||||||||| ||||||| |||||| ||||||||   || ||| |||| |
Db        486 ATGGATTCCTGGAGGAGCCGCTCCGGTCGCTGGAGTCCATCAACACATCCGGCTTGCACA 545

Qy        559 TGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCGGAGTTGCCCTCAG 618
              |||||||||||||||||||| ||||||||||  |||||  | ||||  ||||| | |
Db        546 CGGGGCTGCAGAGGGTGCAGCTGCTGAAGCCCAGCATCCCGAAGCCGGCCCTGCCCGCGG 605

Qy        619 ACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCCAGGAGACCACGT 678
              || || |||||||||||| |||  || ||| |  |||  ||||| ||||| |||||||||
Db        606 ACACGCGCACCATGGAGATCCGCGCCCCCGACGTCCTCATCCCCGGCCAGCAGACCACGT 665

Qy        679 ACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACATTATCAAGTACG 738
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Qy        739 AGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCCAGTGCG 798
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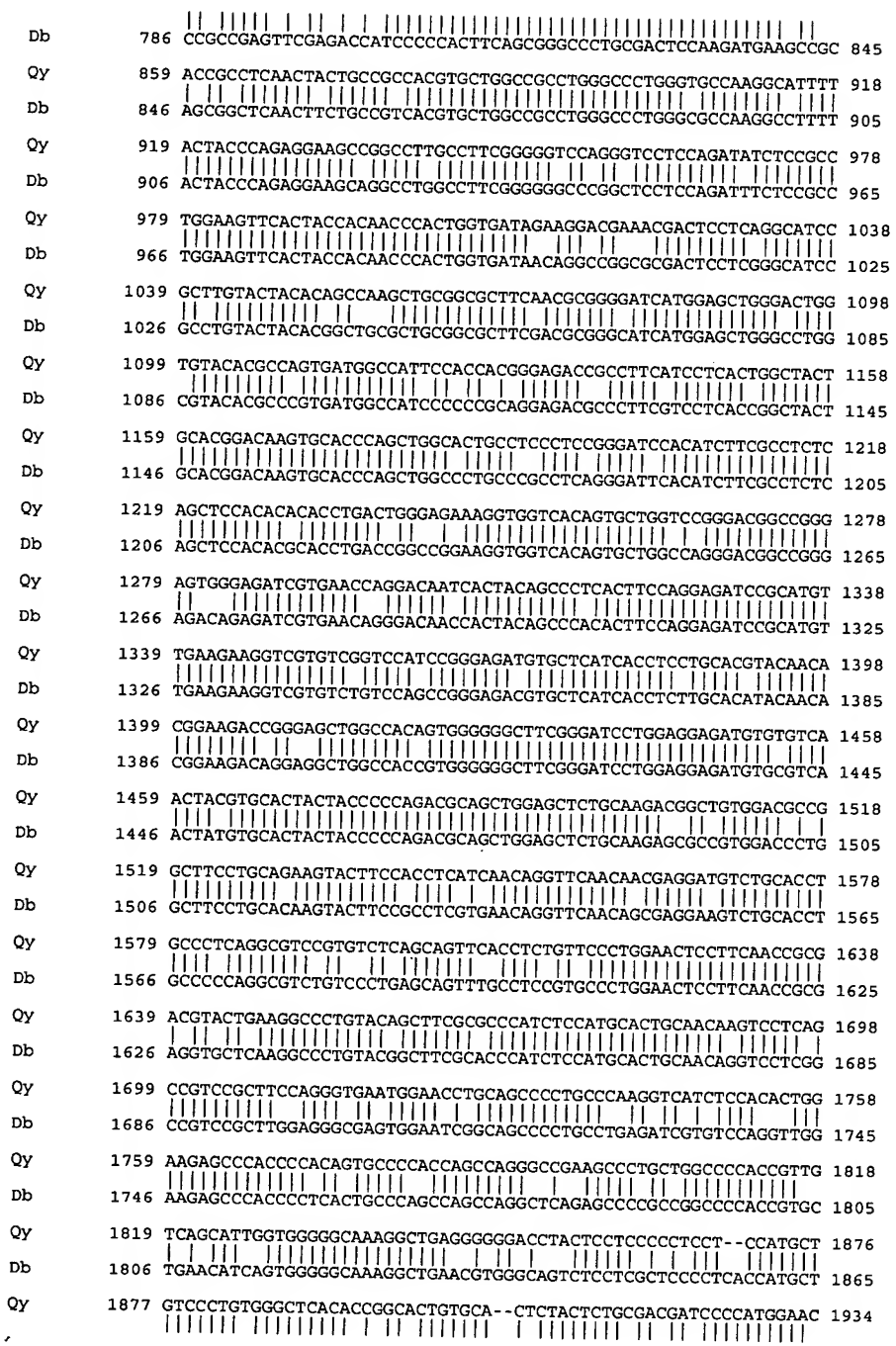

RESULT 9
BOVADBM
LOCUS BOVADBM 2322 bp mRNA linear MAM 26-APR-1993
DEFINITION Bovine adrenal dopamine beta-monooxygenase mRNA, complete cds.
ACCESSION J02890
VERSION J02890.1 GI:162610
KEYWORDS dopamine beta-monooxygenase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Taljanidisz,J., Stewart,L., Smith,A.J. and Klinman,J.P.
TITLE Structure of bovine adrenal dopamine beta-monooxygenase, as deduced from cDNA and protein sequencing: evidence that the membrane-bound form of the enzyme is anchored by an uncleaved signal peptide
JOURNAL Biochemistry 28 (26), 10054-10061 (1989)
MEDLINE 90148928
PUBMED 2620060
COMMENT Original source text: Bovine adrenal medula, cDNA to mRNA.
Draft entry and printed sequence for [1] kindly submitted by C.Mulligan, (18-NOV-89).
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DSKMKPQRLNFCRHVLAAWALGAKAFYYPEEAGLAFGGPGSSRFLRLEVHYHNPLVIT
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ORIGIN

  Query Match           54.2%;  Score 1476.8;  DB 4;  Length 2322;
  Best Local Similarity  80.7%;  Pred. No. 1.5e-265;
  Matches 1818;  Conservative    0;  Mismatches  407;  Indels   27;  Gaps    7;

Qy         19 TGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATCTTCC 78
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Qy         79 TGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCCTATC 138
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Qy        139 ACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACCCAGG 198
              |||||||||||||||| |||||| |||||||||| || |||||  |||||||  | ||||
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Qy        199 AGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCCTGTTTGGGATGT 258
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Qy        259 CCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGACACTG 318
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Qy        319 CCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTGGATCCCCAGCAGG 378
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Db        315 CCTACTTTGGGGATGCCTGGAGTGACCAGAAGGGGCAGGTCCACCTGGACTCCCAGCAGG 374

Qy        379 ACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGC 438
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Db        375 ATTACCAGCTTCTGCGGGCACAGAGGACTCCAGAAGGCCTGTACCTGCTCTTCAAGAGGC 434

Qy        439 CCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACTGTCCACTTGGTCT 498
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Db        435 CTTTTGGCACCTGTGACCCCAACGACTACCTCATCGAGGACGGCACCGTCCACCTGGTGT 494

Qy        499 ACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCCTGCAGA 558
              | ||  |||||||||||||| |||||||| |||||| |||||||||   || ||| |||| |
Db        495 ATGGATTCCTGGAGGAGCCGCTCCGGTCGCTGGAGTCCATCAACACATCCGGCTTGCACA 554

Qy        559 TGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCGGAGTTGCCCTCAG 618
              |||||||||||||||||||| ||||||||||  |||||  | ||||  ||||| | |
Db        555 CGGGGCTGCAGAGGGTGCAGCTGCTGAAGCCCAGCATCCCGAAGCCGGCCCTGCCCGCGG 614

Qy        619 ACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCCAGGAGACCACGT 678
              || |||||||||||||| |||  || ||| |  |||  |||||| ||||| ||||||||||
Db        615 ACACGTGCACCATGGAGATCCGCGCCCCCGACGTCCTCATCCCCGGCCAGCAGACCACGT 674

Qy        679 ACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACATTATCAAGTACG 738
              |||||||||||  | |  ||||| ||  | |||||| | |||||||||||  ||| |||||
Db        675 ACTGGTGCTACGTGACCGAGCTCCCGGACGGCTTCCCCCGGCACCACATCGTCATGTACG 734

Qy        739 AGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCCAGTGCG 798
              |||||||||||||| ||||||| ||||| || || |||||||||| ||||| |||||||
Db        735 AGCCCATCGTCACCGAGGGCAACGAGGCGCTGGTGCACCACATGGAGGTCTTTCAGTGCG 794

Qy        799 CCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAACCCG 858
              || ||||| |     |  ||||||||||||||||||||||||||||||||||||||| ||
Db        795 CCGCCGAGTTTCGAGACCATCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAGCCGC 854

Qy        859 ACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGGCATTTT 918
              | || ||||||| |||||| |||||||||||||||||||||||||| |||||||| ||||
Db        855 AGCGGCTCAACTTCTGCCGTCACGTGCTGGCCGCCTGGGCCCTGGGCGCCAAGGCCTTTT 914

Qy        919 ACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTCCGCC 978
              |||||||||||||||| ||||| |||||||||| || || |||||||||| ||||||||

Db        915 ACTACCCAGAGGAAGCAGGCCTGGCCTTCGGGGGGCCCGGCTCCTCCAGATTTCTCCGCC 974

Qy        979 TGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAAACGACTCCTCAGGCATCC 1038
              |||||||||||||||||||||||||||||||||  ||| ||  |||||||| |||||||
Db        975 TGGAAGTTCACTACCACAACCCACTGGTGATAACAGGCCGGCGCGACTCCTCGGGCATCC 1034

Qy       1039 GCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCATGGAGCTGGGACTGG 1098
              || |||||||||| ||   |||||||||||||| |||||||  |||||||||||||| ||||
Db       1035 GCCTGTACTACACGGCTGCGCTGCGGCGCTTCGACGCGGGCATCATGGAGCTGGGCCTGG 1094

Qy       1099 TGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCATCCTCACTGGCTACT 1158
              |||||||| |||||||||| || || | |||||| |||||| ||||||| |||||||
Db       1095 CGTACACGCCCGTGATGGCCATCCCCCCGCAGGAGACGGCCTTCGTCCTCACCGGCTACT 1154

Qy       1159 GCACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCACATCTTCGCCTCTC 1218
              |||||||||||||||||||||||| ||||  |||| ||||| ||||||||||||||||
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Qy       1219 AGCTCCACACACACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGCCGGG 1278
              |||||||||| |||||||| ||  | |||||||||||||||||| | ||||||||||||
Db       1215 AGCTCCACACGCACCTGACCGGCCGGAAGGTGGTCACAGTGCTGGCCAGGGACGGCCGGG 1274

Qy       1279 AGTGGGAGATCGTGAACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGT 1338
              ||   |||||||||||  |||||| |||||||||| ||||||||||||||||||||||||
Db       1275 AGACAGAGATCGTGAACAGGGACAACCACTACAGCCCACACTTCCAGGAGATCCGCATGT 1334

Qy       1339 TGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACA 1398
              |||||||||||||||  |||||  |||||||| |||||||||||||| |||||  |||||||
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Qy       1399 CGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCA 1458
              ||||||||  ||  |||||||||| |||||||||||||||||||||||||||||||| ||||
Db       1395 CGGAAGACAGGAGGCTGGCCACCGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGCGTCA 1454

Qy       1459 ACTACGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCG 1518
              |||| |||||||||||||||||||||||||||||||||||||||||||  || |||||| | |
Db       1455 ACTATGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGAGCGCCGTGGACCCTG 1514

Qy       1519 GCTTCCTGCAGAAGTACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTCTGCACCT 1578
              ||||||||| |||||||||  |||| | |||||||||||||| |||||| ||||||||||
Db       1515 GCTTCCTGCACAAGTACTTCCGCCTCGTGAACAGGTTCAACAGCGAGGAAGTCTGCACCT 1574

Qy       1579 GCCCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAACCGCG 1638
              |||| |||||||||  ||  || |||||||  |||| || ||||||||||||||||||||
Db       1575 GCCCCCAGGCGTCTGTCCCTGAGCAGTTTGCCTCCGTGCCCTGGAACTCCTTCAACCGCG 1634

Qy       1639 ACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCCTCAG 1698
              | || || |||||||||||| |||||||| |||||||||||||||||||||| |||||| |
Db       1635 AGGTGCTCAAGGCCCTGTACGGCTTCGCACCCATCTCCATGCACTGCAACAGGTCCTCGG 1694

Qy       1699 CCGTCCGCTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGG 1758
              |||||||||||||||| || ||||| | |||||||||||  || || | ||||   |||
Db       1695 CCGTCCGCTTCCAGGGCGAGTGGAATCGGCAGCCCCTGCCTGAGATCGTGTCCAGGTTGG 1754

Qy       1759 AAGAGCCCACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTG 1818
              |||||||||||| ||||||||  |||||||||  |  ||||| || ||||||||||||
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Qy       1819 TCAGCATTGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTC-CATGCTG 1877
              | | |||  |||||||||||||||||  | || |    ||||| | | |||| |
Db       1815 TGAACATCAGTGGGGGCAAAGGCTGAACGTGGGCAGTGTCCTCGCTCCCCTCACCATGCT 1874

Qy       1878 TCCCTGTGGGCTCACACCGGCACTGTGCA--CTCTACTCTGCGACGATCCCCATGGAACA 1935
                |||| |||||||||| | || |||||||  | |||||||| || || |||||||||| |
Db       1875 GTCCTGCGGGCTCACAGCAGCCCTGTGCACCCCCTACTCTGTGAAGACCCCCATGGAATA 1934

Qy       1936 GCCCTGCACGCCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAAT 1995
              |||| |||||           ||||  |||||  ||| |  ||||||||| |||||  |
Db       1935 GCCCAGCACG----------GAGGGCTGGACCAAGCCACCACCTGAGACCAGGGTCCGGT 1984

Qy       1996 CCAGCCTTCTTCCCCCAGGGT-CCCCTGCATGGCTGAGAGGGTGTGGGTGC----CCTGT 2050
              ||||| |||| |||||||||| |||||||||||||| ||   |   |    ||
Db       1985 CCAGCTTTCTCCCCCCAGGGTCCCCCTGCATGGCTGTGACCCTCCCGTGACAACTTTTGC 2044
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Qy       2051 TGACCTACCCTGGACCGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTG 2110
             ||||| ||| || ||  |||||||| |||     || |  | ||||
Db       2045 TGACCCACCGAGGCCCAGGTGGACCAGGAC-----CCTTGCACACCCTTTGACACAGCAT 2099

Qy       2111 CAGGGACAGCCCCGCACAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTG----TTCCGCC 2166
              ||  |  | |||     |  ||| || |||||  | |||  |||||||     ||
Db       2100 AAGAGCAACCCCTTTTGGAAGTCTAGAGTCCAGAGCCCCGAGAGCCCTGCCATCTCGCTG 2159

Qy       2167 TCACTGGGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCAC 2226
              |||||  |  ||| | || |||||||| |  ||| |   || |   |    || || |
Db       2160 GGGCTGGGGGGTGCCCGTCTCCTGGGACACGAGCCACGACCGGACCCCGGCCAGACTCCC 2219

Qy       2227 CGGGAACGCCCCCGCCCCCGCCCCGCTGCTCC 2258
              | |  | |||   ||| || |||    | ||
Db       2220 GGAGCTCTCCCGGCCCCGCGTCCCCAGCCCCC 2251


RESULT 10
BOVDBH
LOCUS       BOVDBH                  1840 bp    mRNA    linear   MAM 27-APR-1993
DEFINITION  Bovine dopamine beta-hydroxylase mRNA, complete cds.
ACCESSION   J05160
VERSION     J05160.1  GI:162962
KEYWORDS    dopamine beta-hydroxylase.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1840)
  AUTHORS   Lewis,E.J., Allison,S., Fader,D., Claflin,V. and Baizer,L.
  TITLE     Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and
            expression in mammalian cells with vaccinia virus vector
  JOURNAL   J. Biol. Chem. 265 (2), 1021-1028 (1990)
  MEDLINE   90110081
   PUBMED   1688549
COMMENT     Original source text: Bovine (adult) adrenal medulla, cDNA to mRNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by E.J.Lewis, 29-NOV-1989.
FEATURES             Location/Qualifiers
     source          1. .1840
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                     /note="dopamine beta-hydroxylase precursor (EC 1.14.17.1)"
                     /codon_start=1
                     /protein_id="AAA30490.1"
                     /db_xref="GI:162963"
                     /translation="MYGTAVAVFLVILVAALQGSAPAESPFPFHIPLDPEGTLELSWN
                     ISYAQETIYFQLLVRELKAGVLFGMSDRGELENADLVVLWTDRDGAYFGDAWSDQKGQ
                     VHLDSQQDYQLLRAQRTPEGLYLLFKRPFGTCDPNDYLIEDGTVHLVYGFLEEPLRSL
                     ESINTSGLHTGLQRVQLLKPSIPKPALPADTRTMEIRAPDVLIPGQQTTYWCYVTELP
                     DGFPRHHIVMYEPIVTEGNEALVHHMEVFQCAAEFETIPHFSGPCDSKMKPQRLNFCR
                     HVLAAWALGAKAFYYPEEAGLAFGGPGSSRFLRLEVHYHNPLVITGRRDSSGIRLYYT
                     AALRRFDAGIMELGLAYTPVMAIPPQETAFVLTGYCTDKCTQLALPASGIHIFASQLH
                     THLTGRKVVTVLARDGRETEIVNRDNHYSPHFQEIRMLKKVVSVQPGDVLITSCTYNT
                     EDRRLATVGGFGILEEMCVNYVHYYPQTQLELCKSAVDPGFLHKYFRLVNRFNSEEVC
                     TCPQASVPEQFASVPWNSFNREVLKALYGFAPISMHCNRSSAVRFQGEWNRQPLPEIV
                     SRLEEPTPHCPASQAQSPAGPTVLNISGGKG"
     sig_peptide     31. .87
                     /note="dopamine beta-hydroxylase signal peptide"
     mat_peptide     88. .1821
                     /product="dopamine beta-hydroxylase"
BASE COUNT      333 a    643 c    547 g    317 t
ORIGIN      212 bp upstream of SstI site.

  Query Match           52.1%;  Score 1419.2;  DB 4;  Length 1840;
  Best Local Similarity   85.7%;  Pred. No. 8.9e-255;
  Matches 1577;  Conservative    0;  Mismatches  263;  Indels    0;  Gaps    0;

Qy         21 CCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATCTTCCTG 80
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                ||| |||||||| |||| ||||| |||| ||||||| |||| || |||||| ||||||||
Db          1 CCCAGCCCCAGCGTGCGCGAGGCGGCCTCCATGTACGGCACCGCGGTGGCCGTCTTCCTG 60

Qy         81 GTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCCTATCAC 140
               |||||||| ||||| |||||||||||||||||||||||   |||||||| ||||||  |||
Db         61 GTCATCCTCGTGGCTGCACTGCAGGGCTCGGCTCCCGCCGAGAGCCCCTTCCCCTTCCAC 120

Qy        141 ATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACCCAGGAG 200
               |||||||||||||| |||||| |||||||||| || ||||||  |||||||  | ||||||
Db        121 ATCCCCCTGGACCCCGAGGGGACCCTGGAGCTGTCCTGGAACATCAGCTATGCGCAGGAG 180

Qy        201 GCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCCTGTTTGGGATGTCC 260
               |||||  |||||||||||||||||  |||||||||||| ||||||||||||||||||||
Db        181 ACCATCTACTTCCAGCTCCTGGTGCGGGAGCTCAAGGCTGGTGTCCTGTTTGGGATGTCG 240

Qy        261 GACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGACACTGCC 320
               ||||| || |||||  ||||| ||  ||  | ||||||||||||||  ||  |||||   |||
Db        241 GACCGAGGGGAGCTGGAGAATGCTGACTTGGTGGTGCTCTGGACTGACAGGGACGGCGCC 300

Qy        321 TATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTGGATCCCCAGCAGGAC 380
               || |||| ||| |||||||||||||||||||||||||||||||  |||||||||  |||||||||
Db        301 TACTTTGGGGATGCCTGGAGTGACCAGAAGGGGCAGGTCCACCTGGACTCCCAGCAGGAT 360

Qy        381 TACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGCCC 440
               |||||||  |||| ||  |||||||| ||||||||||||  |||||| ||||||||||
Db        361 TACCAGCTTCTGCGGGCACAGAGGACTCCAGAAGGCCTGTACCTGCTCTTCAAGAGGCCT 420

Qy        441 TTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACTGTCCACTTGGTCTAC 500
               |||||||||| |||||||| || |||||||| || |||||||| |||||| |||| ||
Db        421 TTTGGCACCTGTGACCCCAACGACTACCTCATCGAGGACGGCACCGTCCACCTGGTGTAT 480

Qy        501 GGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCCTGCAGATG 560
               || |||||||||||||| |||||||| |||||| |||||||   || ||| |||| | ||
Db        481 GGATTCCTGGAGGAGCCGCTCCGGTCGCTGGAGTCCATCAACACATCCGGCTTGCACACG 540

Qy        561 GGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCGGAGTTGCCCTCAGAC 620
               |||||||||||||||||||| |||||||||   |||||| | ||||   |||||  | |||
Db        541 GGGCTGCAGAGGGTGCAGCTGCTGAAGCCCAGCATCCCCAAGCCGGCCCTGCCCGCGGAC 600

Qy        621 GCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCCAGGAGACCACGTAC 680
               || |||||||||| |||  || ||| |  |||  |||||| |||||  ||||||||||||
Db        601 ACGCGCACCATGGAGATCCGCGCCCCCGACGTCCTCATCCCCGGCCAGCAGACCACGTAC 660

Qy        681 TGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACATTATCAAGTACGAG 740
               |||||||| | |  |||| ||  | ||||||  | ||||||||||  |||||||| ||||||||
Db        661 TGGTGCTACGTGACCGAGCTCCCGGACGGCTTCCCCCGGCACCACATCGTCATGTACGAG 720

Qy        741 CCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCCAGTGCGCC 800
               |||||||||||| |||||||  |||||  ||  || ||||||||||  ||||||||||||||||
Db        721 CCCATCGTCACCGAGGGCAACGAGGCGCTGGTGCACCACATGGAGGTCTTCCAGTGCGCC 780

Qy        801 CCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAACCCGAC 860
               |||||  |  ||  |  | |||||||||||||||||||||||||||||||||||||  ||  |
Db        781 GCCGAGTTCGAGACCATCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAGCCGCAG 840

Qy        861 CGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGGCATTTTAC 920
               ||  |||||||  |||||| ||||||||||||||||||||||||||||  ||||||||  ||||||
Db        841 CGGCTCAACTTCTGCCGTCACGTGCTGGCCGCCTGGGCCCTGGGCGCCAAGGCCTTTTAC 900

Qy        921 TACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTCCGCCTG 980
               |||||||||||||| ||||| |||||||||| || || ||||||||||  ||||||||||
Db        901 TACCCAGAGGAAGCAGGCCTGGCCTTCGGGGGGCCCGGCTCCTCCAGATTTCTCCGCCTG 960

Qy        981 GAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAAACGACTCCTCAGGCATCCGC 1040
               |||||||||||||||||||||||||||||||||||  ||| ||  ||||||||||  ||||||||||
Db        961 GAAGTTCACTACCACAACCCACTGGTGATAACAGGCCGGCGCGACTCCTCGGGCATCCGC 1020

Qy       1041 TTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCATGGAGCTGGGACTGGTG 1100
               ||||||||||  ||    |||||||||||||  |||||||  |||||||||||||  |||| |
Db       1021 CTGTACTACACGGCTGCGCTGCGGCGCTTCGACGCGGGCATCATGGAGCTGGGCCTGGCG 1080

Qy       1101 TACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCATCCTCACTGGCTACTGC 1160
               |||||||| |||||||||| || || | ||||||  ||||||  |||||||  |||||||||
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Db       1081 TACACGCCCGTGATGGCCATCCCCCCGCAGGAGACGGCCTTCGTCCTCACCGGCTACTGC 1140

Qy       1161 ACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCACATCTTCGCCTCTCAG 1220
              |||||||||||||||||||||||| |||||  |||| |||||  |||||||||||||||||
Db       1141 ACGGACAAGTGCACCCAGCTGGCCCTGCCCGCCTCAGGGATTCACATCTTCGCCTCTCAG 1200

Qy       1221 CTCCACACACACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGCCGGGAG 1280
              |||||||  |||||||  ||   | ||||||||||||||||||| | ||||||||||||||
Db       1201 CTCCACACGCACCTGACCGGCCGGAAGGTGGTCACAGTGCTGGCCAGGGACGGCCGGGAG 1260

Qy       1281 TGGGAGATCGTGAACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGTTG 1340
              |||||||||||  ||||||  |||||||||||  |||||||||||||||||||||||||
Db       1261 ACAGAGATCGTGAACAGGGACAACCACTACAGCCCACACTTCCAGGAGATCCGCATGTTG 1320

Qy       1341 AAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACACG 1400
              |||||||||||||||  |||||  |||||||||  |||||||||||||  |||||  |||||||||
Db       1321 AAGAAGGTCGTGTCTGTCCAGCCGGGAGACGTGCTCATCACCTCTTGCACATACAACACG 1380

Qy       1401 GAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCAAC 1460
              ||||||  ||  ||||||||  ||||||||||||||||||||||||||||||  ||||||
Db       1381 GAAGACAGGAGGCTGGCCACCGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGCGTCAAC 1440

Qy       1461 TACGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGC 1520
              ||  ||||||||||||||||||||||||||||||||||||||||  ||  ||||||  | |||
Db       1441 TATGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGAGCGCCGTGGACCCTGGC 1500

Qy       1521 TTCCTGCAGAAGTACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTCTGCACCTGC 1580
              ||||||||  |||||||||  |||| | ||||||||||||  ||||||  ||||||||||||
Db       1501 TTCCTGCACAAGTACTTCCGCCTCGTGAACAGGTTCAACAGCGAGGAAGTCTGCACCTGC 1560

Qy       1581 CCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAACCGCGAC 1640
              ||  ||||||||  ||  ||  |||||||  ||||  ||  ||||||||||||||||||||||
Db       1561 CCCCAGGCGTCTGTCCCTGAGCAGTTTGCCTCCGTGCCCTGGAACTCCTTCAACCGCGAG 1620

Qy       1641 GTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCCTCAGCC 1700
              ||  ||  ||||||||||||  |||||||  ||||||||||||||||||||||  ||||||  |||
Db       1621 GTGCTCAAGGCCCTGTACGGCTTCGCACCCATCTCCATGCACTGCAACAGGTCCTCGGCC 1680

Qy       1701 GTCCGCTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAA 1760
              |||||||||||||  ||  |||||  | ||||||||||||  ||  ||  |  ||||  |||||
Db       1681 GTCCGCTTCCAGGGCGAGTGGAATCGGCAGCCCCTGCCTGAGATCGTGTCCAGGTTGGAA 1740

Qy       1761 GAGCCCACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTC 1820
              ||||||||||  ||  |||||  |||||||||  |  |||||  ||  ||||||||||  |
Db       1741 GAGCCCACCCCTCACTGCCCAGCCAGCCAGGCTCAGAGCCCCGCCGGCCCCACCGTGCTG 1800

Qy       1821 AGCATTGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCT 1860
              | |||  |||||||||||||||||  | ||  |  |||||
Db       1801 AACATCAGTGGGGGCAAAGGCTGAACGTGGGCAGTCTCCT 1840
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RESULT 11
BOVDBHZ
LOCUS       BOVDBHZ                 2195 bp    mRNA    linear   MAM 27-APR-1993
DEFINITION  Bovine dopamine beta-hydroxylase mRNA, complete cds.
ACCESSION   J02909
VERSION     J02909.1  GI:162964
KEYWORDS    dopamine beta-hydroxylase.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 2195)
  AUTHORS   Wang,N., Southan,C., DeWolf,W.E. Jr., Wells,T.N., Kruse,L.I. and
            Leatherbarrow,R.J.
  TITLE     Bovine dopamine beta-hydroxylase, primary structure determined by
            cDNA cloning and amino acid sequencing
  JOURNAL   Biochemistry 29 (27), 6466-6474 (1990)
  MEDLINE   91002542
   PUBMED   2207088
COMMENT     Original source text: Bovine, cDNA to mRNA.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9913"
     mRNA            <1. .2195
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BASE COUNT      405 a    764 c    646 g    380 t
ORIGIN
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  Query Match             51.8%;  Score 1412.8;  DB 4;  Length 2195;
  Best Local Similarity   80.7%;  Pred. No. 1.3e-253;
  Matches 1731;  Conservative    0;  Mismatches  387;  Indels   26;  Gaps    6;

Qy        126 CCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTC 185
              ||| ||||||  |||||||||||||||||| |||||| |||||||||| || |||||  ||
Db          1 CCCTTCCCCTTCCACATCCCCCTGGACCCCGAGGGGACCCTGGAGCTGTCCTGGAACATC 60

Qy        186 AGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTC 245
              |||||  | |||||| ||||| | ||||||||||||||||  |||||||||| ||| |
Db         61 AGCTATGCGCAGGAGACCATCTACTTCCAGCTCCTGGTGCGGGAGCTCAAGGCTGGTGTC 120

Qy        246 CTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACC 305
              |||||||||||||| ||||| || ||||| ||||| || ||  | ||||||||||||||
Db        121 CTGTTTGGGATGTCGGACCGAGGGGAGCTGGAGAATGCTGACTTGGTGGTGCTCTGGACT 180

Qy        306 GATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTG 365
              ||  |||||   ||||| |||| ||| |||||||||||||||||||||||| ||||||||
Db        181 GACAGGGACGGCGCCTACTTTGGGGATGCCTGGAGTGACCAGAAGGGGCAGGTCCACCTG 240

Qy        366 GATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTG 425
              ||  |||||||||| |||||||| |||| ||  |||||||| ||||||||||||  ||||
Db        241 GACTCCCAGCAGGATTACCAGCTTCTGCGGGCACAGAGGACTCCAGAAGGCCTGTACCTG 300

Qy        426 CTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACT 485
              || |||||||||| |||||||||| |||||||| || |||||||| || ||||||||
Db        301 CTCTTCAAGAGGCCTTTTGGCACCTGTGACCCCAACGACTACCTCATCGAGGACGGCACC 360

Qy        486 GTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGC 545
              |||||| |||| || ||  |||||||||||||| |||||||  |||||| ||||||||
Db        361 GTCCACCTGGTGTATGGATTCCTGGAGGAGCCGCTCCGGTCGCTGGAGTCCATCAACACA 420

Qy        546 TCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCG 605
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Db        421 TCCGGCTTGCACACGGGGCTGCAGAGGGTGCAGCTGCTGAAGCCCAGCATCCCGAAGCCG 480

Qy        606 GAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGC 665
              |    ||||| | ||| || |||||||||| ||| || ||| |  |||  |||||| ||
Db        481 GCCCTGCCCGCGGACACGCGCACCATGGAGATCCGCGCCCCCGACGTCCTCATCCCCGGC 540

Qy        666 CAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCAC 725
              ||| |||||||||||||||||| | |  ||||| ||  | |||||| | |||||||||
Db        541 CAGCAGACCACGTACTGGTGCTACGTGACCGAGCTCCCGGACGGCTTCCCCCGGCACCAC 600

Qy        726 ATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAA 785
              ||  ||| |||||||||||||||||| |||||||  ||||| || || ||||||||||
Db        601 ATCGTCATGTACGAGCCCATCGTCACCGAGGGCAACGAGGCGCTGGTGCACCACATGGAG 660

Qy        786 GTCTTCCAGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCC 845
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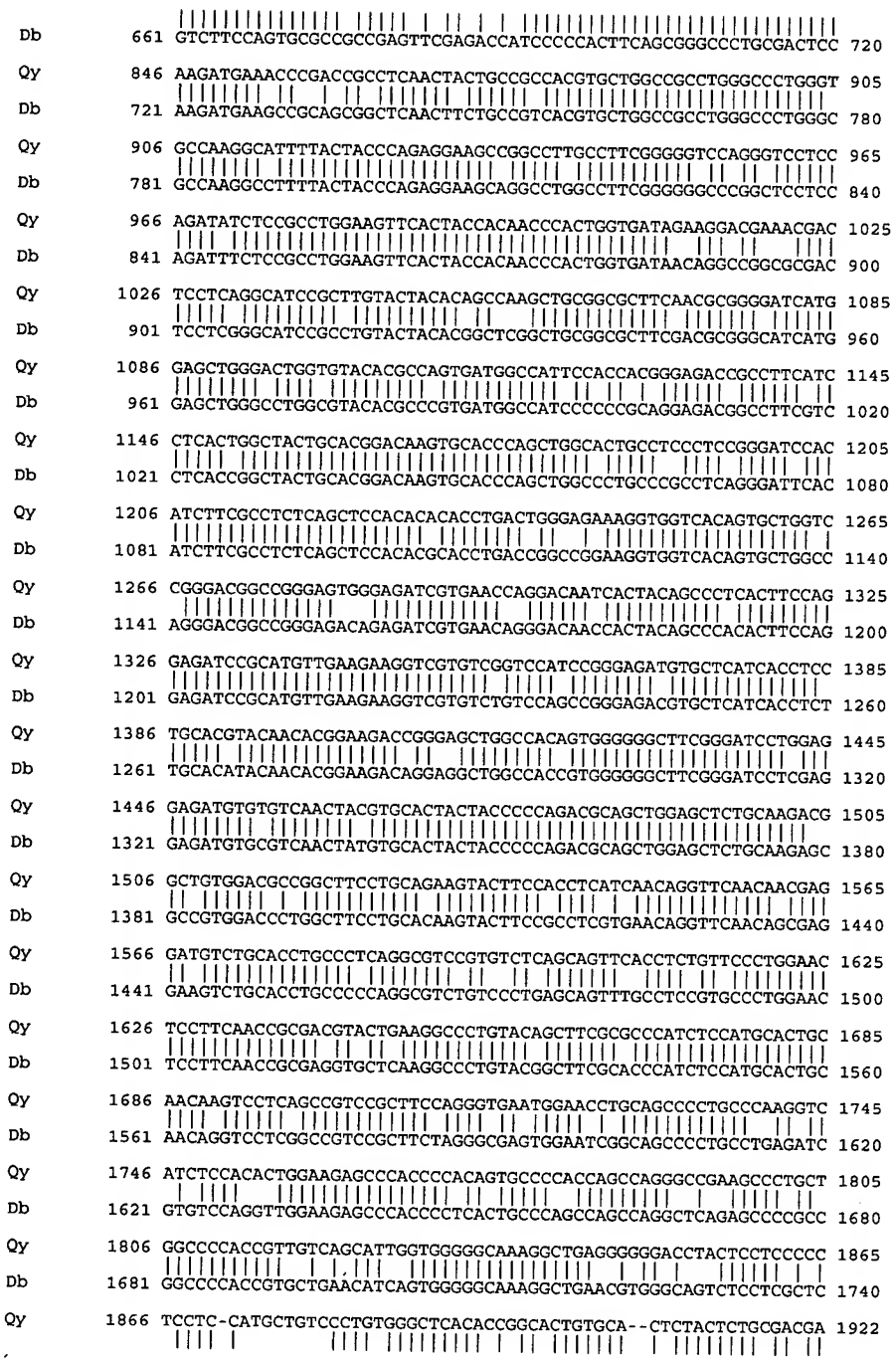

RESULT 12
S50200
LOCUS S50200 2274 bp mRNA linear ROD 11-MAR-2002
DEFINITION Mus musculus dopamine beta-hydroxylase mRNA, complete cds.
ACCESSION S50200
VERSION S50200.1 GI:260872
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2274)
AUTHORS Nakano,T., Kobayashi,K., Saito,S., Fujita,K. and Nagatsu,T.
TITLE Mouse dopamine beta-hydroxylase: primary structure deduced from the cDNA sequence and exon/intron organization of the gene
JOURNAL Biochem. Biophys. Res. Commun. 189 (1), 590-599 (1992)
MEDLINE 93080618
PUBMED 1280432
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 119248] from the original journal article.
This sequence comes from Fig. 5.

FEATURES Location/Qualifiers
source 1. .2274
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/mol_type="mRNA"
/db_xref="taxon:10090"
CDS 285. .2150
/note="This sequence comes from Fig. 2; DBH"
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/protein_id="AAB24330.1"
/db_xref="GI:260873"
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KDYVIEDDTVHLVYGILEEPFQSLEAINTSGLHTGLLRVQLLKSEVPTPSMPEDVQTM
DIRAPDILIPDNEQTYWCYITELPPRFPRHHIIMYEAIVTEGNEALVHHMEVFQCAAE
SEDFPQFNGPCDSKMKPDRLNYCRHVLAAWALGAKAFYYPKEAGVPFGGPGSSPFLRL
EVHYHNPRKIQGRQDSSGIRLPYTATLRRYDAGIMELGLVYTPLMAIPPQETAFVLTG
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SAVDDGFLQKYFHMVNRFSSEEVCTCPQASVPQQFSSVPWNSFNRNMLKALYDYAPIS
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BASE COUNT 510 a 685 c 594 g 485 t
ORIGIN

Query Match 45.4%; Score 1236.8; DB 10; Length 2274;
Best Local Similarity 79.5%; Pred. No. 9.6e-221;
Matches 1463; Conservative 0; Mismatches 377; Indels 0; Gaps 0;

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Qy          5 TCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGC 64
Db        311 TTGTTGGAGCAGCCTCCCAAGCCCCAGTGTCCGTGAGGCGGCTTCCATGTACGGCACTGC 370

Qy         65 AGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAG 124
Db        371 TGTGGCCATCTTCCTGGTCATCCTGGTGGCTGCACTGCGGGGCTCGGAGCCTCCAGAGAG 430

Qy        125 CCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGT 184
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Qy        185 CAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGT 244
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Qy        245 CCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGAC 304
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Qy        305 CGATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCT 364
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Qy        365 GGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCT 424
Db        671 GGATTCCCAGCAAGACTACCAGCTGCTCCAGGCACAGAGGACTCGAGATGGCCTGTCCCT 730

Qy        425 GCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCAC 484
Db        731 GCTCTTCAAGAGGCCCTTTGTCACCTGTGACCCCAAGGATTATGTCATTGAGGATGACAC 790

Qy        485 TGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGG 544
Db        791 TGTCCATCTAGTGTATGGGATCTTGGAAGAGCCATTTCAGTCGCTGGAGGCCATCAACAC 850

Qy        545 CTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACC 604
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Qy        605 GGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAG 664
Db        911 ATCCATGCCTGAGGATGTACAAACCATGGATATCCGGGCTCCTGACATCCTCATCCCCGA 970

Qy        665 CCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCA 724
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Qy        725 CATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGA 784
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Qy        845 CAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGG 904
Db       1151 CAAAATGAAGCCTGACCGACTCAACTACTGCCGGCACGTGCTGGCAGCATGGGCCCTGGG 1210

Qy        905 TGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTC 964
Db       1211 TGCCAAGGCATTTTACTACCCAAAAGAAGCTGGTGTTCCCTTTGGGGGCCCGGGGTCCTC 1270

Qy        965 CAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAAACGA 1024
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Qy       1025 CTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCAT 1084
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Qy       1085 GGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCAT 1144
Db       1391 GGAGCTCGGACTGGTGTATACACCCTTGATGGCCATCCCCCCTCAGGAGACTGCCTTTGT 1450

Qy       1145 CCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCA 1204
Db       1451 GTTGACCGGCTACTGCACAGACAAGTGCACCCAGATGGCACTGCAGGACTCCGGAATCCA 1510

Qy       1205 CATCTTCGCCTCTCAGCTCCACACACACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGT 1264
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Qy       1325 GGAGATCCGCATGTTGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCACCTC 1384
Db       1631 GGAGATCAGAATGCTGAAGAAGGTTGTGACAGTCTACCCGGGGGACGTACTCATCACTTC 1690

Qy       1385 CTGCACGTACAACACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGA 1444
Db       1691 ATGCACATACAACACAGAAAACAAGACGCTGGCCACAGTGGGGGGGTTTGGAATCTTGGA 1750

Qy       1445 GGAGATGTGTGTCAACTACGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGAC 1504
Db       1751 GGAGATGTGTGTCAACTATGTGCACTACTACCCCCAGACAGAGCTGGAACTCTGCAAGAG 1810

Qy       1505 GGCTGTGGACGCCGGCTTCCTGCAGAAGTACTTCCACCTCATCAACAGGTTCAACAACGA 1564
Db       1811 TGCCGTGGACGACGGCTTCCTACAGAAATACTTCCACATGGTAAACAGGTTCAGCAGTGA 1870

Qy       1565 GGATGTCTGCACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAA 1624
Db       1871 GGAGGTCTGCACCTGCCCTCAGGCCTCAGTCCCCCAGCAGTTCTCCTCCGTGCCCTGGAA 1930

Qy       1625 CTCCTTCAACCGCGACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTG 1684
Db       1931 CTCTTTCAATCGGAATATGCTCAAGGCTCTGTATGACTACGCCCCTATCTCCATGCATTG 1990

Qy       1685 CAACAAGTCCTCAGCCGTCCGCTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGT 1744
Db       1991 CAACAAGACTTCTGCTGTCCGCTTCCCGGGTGAGTGGAACCTGCAGCCTTTGCCTAAGAT 2050

Qy       1745 CATCTCCACACTGGAAGAGCCCACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGC 1804
Db       2051 CACCTCCACGCTGGAAGAACCCACCCCACGCTGCCCCATCCGACAGACTCAGAGCCCCGC 2110

Qy       1805 TGGCCCCACCGTTGTCAGCATTGGTGGGGGCAAAGGCTGA 1844
Db       2111 TAACCCCACTGTGCCCATCACAACAGGAGGCAGATGCTGA 2150
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RESULT 13
RATDOPBHY

LOCUS	RATDOPBHY 2443 bp mRNA linear ROD 12-JUN-1993
DEFINITION	Rattus norvegicus dopamine beta-hydroxylase mRNA, complete cds.
ACCESSION	L12407
VERSION	L12407.1 GI:294539
KEYWORDS	dopamine beta-hydroxylase.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 2443)
AUTHORS	McMahon,A., Geertman,R. and Sabban,E.L.
TITLE	Rat dopamine beta-hydroxylase: molecular cloning and characterization of the cDNA and regulation of the mRNA by reserpine

```
  JOURNAL   J. Neurosci. Res. 25 (3), 395-404 (1990)
  MEDLINE   90219125
   PUBMED   2325165
COMMENT     Original source text: Rattus norvegicus (strain Sprague-Dawley)
            pheochromacytoma tumor cDNA to mRNA.
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                     /mol_type="mRNA"
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     CDS             7. .1869
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                     CTDRCTQMALPKSGIRIFASQLHTHLTGRKVITVLARDGQQREVVNRDNHYSPHFQEI
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     3'UTR           1870. .2443
     polyA_signal    2309. .2314
     polyA_signal    2424. .2429
BASE COUNT      610 a    725 c    595 g    513 t
ORIGIN

  Query Match           44.7%;  Score 1219.4;  DB 10;  Length 2443;
  Best Local Similarity   76.9%;  Pred. No. 1.7e-217;
  Matches 1513;  Conservative    0;  Mismatches  451;  Indels    3;  Gaps    2;

Qy         15 AGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATC 74
              ||||| ||| |||||||| | || ||||| || | ||||||  |||| || |||||||||
Db         40 AGCCTCCCCAGCCCCAGCGTCCGTGAGGCGGCTTCCATGTATGGCACTGCTGTGGCCATC 99

Qy         75 TTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCC 134
              |||||||||||||||||||| ||||||||||||||||  || |  |||||||| ||||
Db        100 TTCCTGGTCATCCTGGTGGCTGCACTGCAGGGCTCGGAGCCTCCGGAGAGCCCCTTCCCT 159

Qy        135 TATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACC 194
              || |||||||||||||||| || ||| |  | |||||||| ||||| ||||||||   |
Db        160 TACCACATCCCCCTGGACCCTGAAGGGACTTTAGAGCTCTCGTGGAACGTCAGCTATGAC 219

Qy        195 CAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCCTGTTTGGG 254
              ||||||  |||||| |||||||||| |||||   |||  | ||||||  |||||||| ||
Db        220 CAGGAGATCATCCACTTCCAGCTCCAGGTGCAAGGGCCGAGGGCTGGGGTCCTGTTCGGA 279

Qy        255 ATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGAC 314
              ||||| || || || ||| | |||||||||||| |||||  |||||||||| || ||||||
Db        280 ATGTCGGATCGAGGTGAGATGGAGAACGCAGACCTCGTCATGCTCTGGACTGACGGGGAC 339

Qy        315 ACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTGGATCCCCAG 374
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Db        340 AGGACCTACTTTGCGGACGCCTGGAGTGACCAGAAAGGGCAGATCCATCTGGATACCCAT 399

Qy        375 CAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGCTTTTCAAG 434
              |||||||||||||||| ||||  ||||||    || |  |||| |||||||  ||||||
Db        400 CAGGACTACCAGCTGCTCCAGGCACAGAGGGTGTCAAACAGCCTATCCCTGCTCTTCAAG 459

Qy        435 AGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACTGTCCACTTG 494
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Db        460 AGGCCCTTTGTCACCTGCGACCCCAAGGATTATGTCATTGAGGATGACACTGTCCATCTA 519

Qy        495 GTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCCTG 554
              || || |||||||||||||||| |||| ||| ||||||||||||||  ||| |||||

Db        520 GTGTATGGGATCCTGGAGGAGCCATTCCAGTCCCTGGAGGCCATCAACACCTCAGGCCTA 579

Qy        555 CAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCGGAGTTGCCC 614
              || | ||| || |||  ||||||||| |||||||| |  || ||  || |  ||||
Db        580 CATACGGGACTACAGCAGGTGCAGCTTCTGAAGCCTGAGGTCTCCACTCCAGCCATGCCT 639

Qy        615 TCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCCAGGAGACC 674
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Db        640 GCGGATGTACAAACCATGGATATCCGGGCTCCTGACGTCCTCATCCCCAGCACTGAGACC 699

Qy        675 ACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACATTATCAAG 734
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Db        700 ACATACTGGTGCTATATCACTGAGCTACCCCTACACTTCCCCCGACACCACATCATCATG 759

Qy        735 TACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCCAG 794
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Db        760 TATGAGGCCATTGTCACGGAGGGCAATGAGGCCCTGGTGCACCACATGGAGGTCTTCCAA 819

Qy        795 TGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAA 854
              ||  |   |||  ||  | |||||   |||| ||| |||||||||||||||||||||
Db        820 TGTACAAATGAGTCTGAGGCCTTCCCCATGTTCAACGGACCCTGCGACTCCAAGATGAAA 879

Qy        855 CCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGGCA 914
              || ||| | |||||||||||  |||||||||||||| || ||||||||||  |||||||||
Db        880 CCTGACAGACTCAACTACTGTCGCCACGTGCTGGCGGCATGGGCCCTGGGCGCCAAGGCA 939

Qy        915 TTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTC 974
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Db        940 TTTTACTACCCAGAAGAAGCCGGTGTCCCTTTGGGGAGCTCAGGATCCTCCCGGTTTCTC 999

Qy        975 CGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGAAACGACTCCTCAGGC 1034
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Db       1000 CGACTGGAAGTTCATTACCACAATCCACGGAATATACAAGGCCGGCGCGACTCCTCTGGC 1059

Qy       1035 ATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCATGGAGCTGGGA 1094
              |||||  |  |||||||||| |  || || | |    | || || |||||||||| |||
Db       1060 ATCCGTCTACACTACACAGCTAGTCTCCGACCCAATGAGGCAGGCATCATGGAGCTTGGA 1119

Qy       1095 CTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCATCCTCACTGGC 1154
              |||||||||||||| |||||||||| || || | ||||||| |||| |  | ||||||
Db       1120 CTGGTGTACACGCCCTTGATGGCCATCCCCCCTCAGGAGACCACCTTTGTTTTGACTGGC 1179

Qy       1155 TACTGCACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCACATCTTCGCC 1214
              |||||||| |||| |||||||||| |||||||||||    || || |||| |||||| |||
Db       1180 TACTGCACAGACAGGTGCACCCAGATGGCACTGCCGAAATCTGGAATCCGCATCTTTGCC 1239

Qy       1215 TCTCAGCTCCACACACACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGC 1274
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Db       1240 TCACAGCTCCACACGCACCTGACCGGCAGGAAGGTGATTACTGTGCTCGCCAGGGATGGC 1299

Qy       1275 CGGGAGTGGGAGATCGTGAACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGC 1334
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Db       1300 CAACAGAGGGAAGTGGTGAACAGAGACAACCACTACAGCCCCCACTTTCAGGAGATCAGA 1359

Qy       1335 ATGTTGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTAC 1394
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Db       1360 ATGCTGAAGAATGCTGTGACTGTCCACCAGGGGGATGTCCTCATCACTTCGTGCACATAC 1419

Qy       1395 AACACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGT 1454
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Db       1420 AACACAGAAAACAGGACAATGGCCACAGTGGGGGGGTTTGGAATCTTGGAGGAGATGTGC 1479

Qy       1455 GTCAACTACGTGCACTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGAC 1514
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Db       1480 GTCAACTACGTCCACTACTACCCCAAAACAGAGCTGGAGCTCTGCAAGAGTGCCGTGGAT 1539

Qy       1515 GCCGGCTTCCTGCAGAAGTACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTCTGC 1574
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Db       1540 GATGGCTTCCTGCAGAAATACTTCCACATAGTAAACCGGTTCGGCAATGAGGAGGTCTGC 1599

Qy       1575 ACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAAC 1634
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Qy       1635 CGCGACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCC 1694
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Qy       1755 CTGGAAGAGCCCACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCCACC 1814
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Db       1780 GTGGAAGAACCCGACCCACGCTGCCCCATCCGACAGACTCGGGGACCCGCCGGCCCCTTC 1839

Qy       1815 GTTGTCAGCATTGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATG 1874
             |||||||  ||  |   ||  ||||  |   ||||   |       |  ||  |   ||  ||||||   |
Db       1840 GTTGTCATCACTCACGGAGGCAGACACTGA--GTAATTGTTCTTCAGCCTCTCCTCGTTT 1897

Qy       1875 CTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATC-CCCATGGAA 1933
                 ||   |||||||||  ||  ||  |||  ||||  |  ||      |||  |   ||||  |||
Db       1898 TGTCCCTACTGGGCTCACTCCAGCTCTGCGCACCCCACATGAAGACCCCCTTCCATAGAA 1957

Qy       1934 CAGCCCTGCACGCCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTG 1980
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Db       1958 TAGTGCTGTTCACCTAGGAGGAGGGGGTATCACCTTGGAGACACCTG 2004
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RESULT 14
HSDBH12
LOCUS HSDBH12 1092 bp DNA linear PRI 04-MAY-1990
DEFINITION Human DNA for dopamine beta-hydroxylase exon 12 (EC 1.14.17.1).
ACCESSION X13268
VERSION X13268.1 GI:30462
KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1092)
AUTHORS Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation
JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
MEDLINE 89160241
PUBMED 2922261
REFERENCE 2 (bases 1 to 1092)
AUTHORS Nagatsu,T.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="9q34"
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/note="Intron XI (ca 0.9 kb)"
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/note="Exon 12"
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/note="pot. polyA signal"
misc_feature 999. .1004
/note="pot. alt. polyA signal"
misc_feature 1026. .1030
/note="pot. alt. polyA signal"
BASE COUNT 200 a 353 c 322 g 217 t
ORIGIN

Query Match 37.3%; Score 1016.8; DB 9; Length 1092;
Best Local Similarity 99.8%; Pred. No. 1.3e-179;
Matches 1018; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1706 CTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 1765
             |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTGCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 62

Qy       1766 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 1825
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 122

Qy       1826 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 1885
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Db         123 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 182

Qy       1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 1945
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Db         183 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 242

Qy       1946 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 2005
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Db         243 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 302

Qy       2006 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 2065
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Db         303 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 362

Qy       2066 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCA 2125
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Db         363 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCTGCA 422

Qy       2126 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 2185
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Db         423 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 482

Qy       2186 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 2245
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Db         483 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 542

Qy       2246 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 2305
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Db         543 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 602

Qy       2306 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 2365
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Db         603 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 662

Qy       2366 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 2425
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Db         663 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 722

Qy       2426 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 2485
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Db         723 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 782

Qy       2486 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 2545
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Db         783 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 842

Qy       2546 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 2605
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Db         843 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 902

Qy       2606 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 2665
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RESULT 15
AC000404/c
LOCUS AC000404 46651 bp DNA linear PRI 29-MAY-1997

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DEFINITION  Genomic sequence from Human 9q34, complete sequence.
ACCESSION   AC000404
VERSION     AC000404.1  GI:2133857
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46651)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H. and Lander,E.S.
  TITLE     Genomic sequence from Human 9q34
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 46651)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Brown,K., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 46651)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 29, 1997 this sequence version replaced gi:1929451.
            The Staden databases, finishing information, and all
            chromatographic files used in the assembly of this clone are
            available from our anonymous ftp site.

            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html.
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     repeat_region   complement(2945. .3017)
                     /rpt_family="MIR"
     repeat_region   complement(3040. .3239)
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     repeat_region   8307. .8745
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Query Match 37.3%; Score 1016.8; DB 9; Length 46651;
Best Local Similarity 99.8%; Pred. No. 6.8e-180;

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Qy       1706 CTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 1765
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Db      28060 CTTGCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 28001

Qy       1766 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 1825
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Db      28000 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 27941

Qy       1826 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 1885
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Db      27940 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 27881

Qy       1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 1945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27880 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 27821

Qy       1946 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 2005
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Db      27820 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 27761

Qy       2006 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 2065
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Db      27760 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 27701

Qy       2066 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCA 2125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      27700 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCTGCA 27641

Qy       2126 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 2185
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Db      27640 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 27581

Qy       2186 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 2245
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Db      27580 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 27521

Qy       2246 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 2305
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Qy       2306 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 2365
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Db      27460 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 27401

Qy       2366 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 2425
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Db      27400 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 27341

Qy       2426 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 2485
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Qy       2486 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 2545
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Db      27280 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 27221

Qy       2546 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 2605
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Qy       2606 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 2665
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Db      27160 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 27101

Qy       2666 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 2725
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Db      27100 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 27041
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RESULT 16
AL365494

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LOCUS       AL365494               53242 bp    DNA     linear   PRI 07-APR-2003
DEFINITION  Human DNA sequence from clone RP11-317B10 on chromosome 9, complete
            sequence.
ACCESSION   AL365494
VERSION     AL365494.17  GI:29603316
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 53242)
  AUTHORS   Barker,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-APR-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Apr 7, 2003 this sequence version replaced gi:27817269.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
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            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr9
            RP11-317B10 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
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Qy       1706 CTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 1765
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Db      32933 CTTGCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 32992

Qy       1766 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 1825
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32993 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 33052
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Qy       1826 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 1885
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33053 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 33112

Qy       1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 1945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33113 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 33172

Qy       1946 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 2005
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33173 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 33232

Qy       2006 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 2065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33233 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 33292

Qy       2066 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCA 2125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      33293 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCTGCA 33352

Qy       2126 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 2185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33353 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 33412

Qy       2186 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 2245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33413 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 33472

Qy       2246 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 2305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33473 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 33532

Qy       2306 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 2365
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Db      33533 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 33592

Qy       2366 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 2425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33593 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 33652

Qy       2426 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 2485
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Db      33653 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 33712

Qy       2486 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 2545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33713 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 33772

Qy       2546 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 2605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33773 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 33832

Qy       2606 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 2665
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Db      33833 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 33892

Qy       2666 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 2725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33893 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 33952
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RESULT 17
AL954350_3/c
WPCOMMENT
Sequence split into 6 fragments LOCUS AL954350 Accession AL954350

Fragment Name	Begin	End
AL954350_0	1	110000
AL954350_1	100001	210000
AL954350_2	200001	310000
AL954350_3	300001	410000
AL954350_4	400001	510000
AL954350_5	500001	539816

Continuation (4 of 6) of AL954350 from base 300001 (AL954350 Homo sapiens chromosome 9 c

Query Match 37.3%; Score 1016.8; DB 2; Length 110000;
Best Local Similarity 99.8%; Pred. No. 5.9e-180;
Matches 1018; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1706 CTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 1765
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Db      21303 CTTGCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 21244

Qy       1766 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCCACCGTTGTCAGCAT 1825
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21243 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCCACCGTTGTCAGCAT 21184

Qy       1826 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 1885
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Db      21183 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 21124

Qy       1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 1945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21123 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 21064

Qy       1946 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 2005
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Db      21063 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 21004

Qy       2006 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 2065
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Db      21003 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 20944

Qy       2066 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCA 2125
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Db      20943 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCTGCA 20884

Qy       2126 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 2185
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Db      20883 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 20824

Qy       2186 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 2245
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Db      20823 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 20764

Qy       2246 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 2305
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Db      20763 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 20704

Qy       2306 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 2365
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Db      20703 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 20644

Qy       2366 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 2425
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Db      20643 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAGATATTTTCGCCCACCT 20584

Qy       2426 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 2485
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Db      20583 AAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCGGGGC 20524

Qy       2486 TTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGCCGGT 2545
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Qy       2546 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 2605
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Db      20463 GGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTCTGCC 20404

Qy       2606 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 2665
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Db      20403 ACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTCATCT 20344

Qy       2666 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 2725
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Db      20343 GTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGCTGGC 20284
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WPCOMMENT
  Sequence split into 6 fragments  LOCUS AL954350 Accession AL954350
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     AL954350_1        100001    210000
     AL954350_2        200001    310000
     AL954350_3        300001    410000
     AL954350_4        400001    510000
     AL954350_5        500001    539816
LOCUS       AL954350              539816 bp    DNA     linear   HTG 02-DEC-2002
DEFINITION  Homo sapiens chromosome 9 clone RP13-32M24, *** SEQUENCING IN
            PROGRESS ***, 12 unordered pieces.
ACCESSION   AL954350
VERSION     AL954350.4  GI:26185663
KEYWORDS    HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 539816)
  AUTHORS   Skuce,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Dec 6, 2002 this sequence version replaced gi:25809651.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bB32M24
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 213719 bases at least Q40
            Consensus quality: 214110 bases at least Q30
            Consensus quality: 214326 bases at least Q20
            Insert size: 538716; sum-of-contigs
            Insert size: 214531; 5.7% error; agarose-fp
            Quality coverage: 3.38x in Q20 bases; sum-of-contigs Quality
            coverage: 8.80x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 12 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    14160: contig of 14160 bp in length
            *    14161    14260: gap of 100 bp
            *    14261    19871: contig of 5611 bp in length
            *    19872    19971: gap of 100 bp
            *    19972    30753: contig of 10782 bp in length
            *    30754    30853: gap of 100 bp
            *    30854   149524: contig of 118671 bp in length
            *   149525   149624: gap of 100 bp
            *   149625   354235: contig of 204611 bp in length
            *   354236   354335: gap of 100 bp
            *   354336   404612: contig of 50277 bp in length
            *   404613   404712: gap of 100 bp
            *   404713   420328: contig of 15616 bp in length
            *   420329   420428: gap of 100 bp
            *   420429   440973: contig of 20545 bp in length
            *   440974   441073: gap of 100 bp
            *   441074   476711: contig of 35638 bp in length
            *   476712   476811: gap of 100 bp
            *   476812   519484: contig of 42673 bp in length
            *   519485   519584: gap of 100 bp
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                     fragment_chain:2"
     misc_feature    519585. .523931
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     misc_feature    524032. .539816
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  Matches 1017;  Conservative    0;  Mismatches    3;  Indels    4;  Gaps    1;

Qy       1706 CTTCCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 1765
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Db      20812 CTTGCAGGGTGAATGGAACCTGCAGCCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCC 20871

Qy       1766 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 1825
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Db      20872 CACCCCACAGTGCCCCACCAGCCAGGGCCGAAGCCCTGCTGGCCCCACCGTTGTCAGCAT 20931

Qy       1826 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 1885
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Db      20932 TGGTGGGGGCAAAGGCTGAGGGGGGACCTACTCCTCCCCCTCCTCCATGCTGTCCCTGTG 20991

Qy       1886 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCACG 1945
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Db      20992 GGCTCACACCGGCACTGTGCACTCTACTCTGCGACGATCCCCATGGAACAGCCCTGCATG 21051

Qy       1946 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 2005
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Db      21052 CCCAGGATGAAGGGGCCAGACCACGCCCCTGCCTGAGACCACGGTCCAATCCAGCCTTCT 21111

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Db      21112 TCCCCCAGGGTCCCCTGCATGGCTGAGAGGGTGTGGGTGCCCTGTTGACCTACCCTGGAC 21171

Qy       2066 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCA 2125

Db      21172 CGAGTGGACCACGACCTCGTCCATTTAAACCCGGCTGACTCAGTGCAGGGACAGCCTGCA 21231

Qy       2126 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 2185

Db      21232 CAGTGGTCCAGGGTCCAGCCCTCCGCCAGCCCTGTTCCGCCTCACTGGGTGTGGCCTGGC 21291

Qy       2186 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 2245

Db      21292 TTCTGGGACAGGCACCATGCTGGGCCGGGGTGTGGAATCACCGGGAACGCCCCCGCCCCC 21351

Qy       2246 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 2305

Db      21352 GCCCCGCTGCTCCCGGTGTGCAGCGGGTGCGGGTGCCGCTTAAACATTTCCCTGCTGAGT 21411

Qy       2306 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 2365

Db      21412 GGCTCGTGTTTCACAGTGGGCGGCTTCCCTGCGACGGAGGCAGGACCAGGCATTTAGCTA 21471

Qy       2366 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGT----AAACAGATATTTTCGCCC 2421

Db      21472 GTTAGAGACTCGCCTGGGAAATTGCTCCATTCCTGAGTAAACAAACAGATATTTTCGCCC 21531

Qy       2422 ACCTAAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCG 2481

Db      21532 ACCTAAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAGGCGGCAAAGATCCAGCG 21591

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Db      21592 GGGCTTCTGGGCGCCGGTTCCACGTGGGGTGGAATTATTAGCACCAGCTTGCTTCTCTGC 21651

Qy       2542 CGGTGGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTC 2601

Db      21652 CGGTGGGGCCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGCTTTCCGCGTGGTTC 21711

Qy       2602 TGCCACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTC 2661

Db      21712 TGCCACTTAGGGAGTGTGCCTTGGGCGGGCCATTTCACATTCCTGACCCTCACTTTTCTC 21771

Qy       2662 ATCTGTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGC 2721

Db      21772 ATCTGTAAAACCAGGCTGATGCCGTGCGGGCTAATGAGCCAATAAAGCTCACACTTGGGC 21831

Qy       2722 TGGC 2725

Db      21832 TGGC 21835


RESULT 19
HSDBH1
LOCUS       HSDBH1                  2037 bp    DNA     linear   PRI 04-MAY-1990
DEFINITION  Human DNA for dopamine beta-hydroxylase exon 1 (EC 1.14.17.1).
ACCESSION   X13257
VERSION     X13257.1  GI:30459
KEYWORDS    alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2037)
  AUTHORS   Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
  TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
            different 3'-terminal regions are produced through alternative
            polyadenylation
  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 2037)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
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Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120

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Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180

Db       1820 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 1879

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240

Db       1880 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 1939

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300

Db       1940 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 1999

Qy        301 GGACCGATGGGGACACTGCCTATTTTGCGG 330

Db       2000 GGACCGATGGGGACACTGCCTATTTTGCGG 2029


RESULT 20
AC001227/c
LOCUS       AC001227                37584 bp    DNA     linear   PRI 29-MAY-1997
DEFINITION  Genomic sequence from Human 9q34, complete sequence.
ACCESSION   AC001227
VERSION     AC001227.1  GI:2133860
KEYWORDS    HTG.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37584)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H. and Lander,E.S.
  TITLE     Genomic sequence from Human 9q34
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 37584)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Brown,K., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 37584)
  AUTHORS   Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
            Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
            Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J.,
            Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzie,J.,
            Marquis,N., McDermott,J., Moloney,N., Morrow,J., Nachman,A.,
            Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
            Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 29, 1997 this sequence version replaced gi:1932719.
            The Staden databases, finishing information, and all
            chromatographic files used in the assembly of this clone are
            available from our anonymous ftp site.

            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html.
FEATURES             Location/Qualifiers
     source          1. .37584
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="9q34"
                     /clone="30E11"
                     /clone_lib="Alan Buckler -- per comm"
     repeat_region   1090. .1387
                     /rpt_family="AluSx"
     repeat_region   complement(2030. .2138)
                     /rpt_family="MIR"
     repeat_region   complement(2889. .2982)
                     /rpt_family="(CA)n"
     repeat_region   4846. .4896
                     /rpt_family="MIR"
     repeat_region   4915. .4985
                     /rpt_family="MIR"
     repeat_region   6645. .6697
                     /rpt_family="MIR"
     repeat_region   complement(7453. .7572)
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     repeat_region   complement(8666. .8798)
                     /rpt_family="FLAM_C"
     repeat_region   complement(12619. .12664)
                     /rpt_family="(GGAA)n"
     repeat_region   15236. .15544
                     /rpt_family="AluJo"
     repeat_region   16117. .16161
                     /rpt_family="(CA)n"
     repeat_region   16443. .16522
                     /rpt_family="MIR"
     repeat_region   16911. .17089
                     /rpt_family="MLT1D"
     repeat_region   17081. .17337
                     /rpt_family="MLT1D"
     repeat_region   18852. .18905
                     /rpt_family="MIR"
     repeat_region   complement(19155. .19734)
                     /rpt_family="L1MB3"
     repeat_region   20662. .21018
                     /rpt_family="THE1B"
     repeat_region   21019. .21281
                     /rpt_family="MSTA"
     repeat_region   21283. .22505
                     /rpt_family="MST-INTERNAL"
     repeat_region   22679. .23075
                     /rpt_family="THE1B-INTERNAL"
     repeat_region   23078. .23461
                     /rpt_family="MSTA"
     repeat_region   complement(23656. .23945)
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     repeat_region   complement(24124. .24503)
                     /rpt_family="THE1B"
     repeat_region   26195. .26504
                     /rpt_family="AluY"
     repeat_region   complement(26624. .27097)
                     /rpt_family="MER44C"
     repeat_region   27098. .27400
                     /rpt_family="AluSx"
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     repeat_region   complement(27435. .27489)
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     repeat_region   complement(28266. .28304)
                     /rpt_family="AT_rich"
     repeat_region   complement(28515. .28703)
                     /rpt_family="MIR"
     repeat_region   29099. .29397
                     /rpt_family="AluSq"
     repeat_region   complement(31375. .31417)
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     repeat_region   31620. .31730
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     repeat_region   complement(32613. .32691)
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     repeat_region   33568. .33656
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     repeat_region   35983. .36061
                     /rpt_family="MIR"
     repeat_region   complement(36489. .36578)
                     /rpt_family="(GAAA)n"
     repeat_region   complement(36493. .36537)
                     /rpt_family="(GA)n"
     repeat_region   36677. .36825
                     /rpt_family="MIR"
     repeat_region   37141. .37208
                     /rpt_family="MIR"
     repeat_region   37345. .37584
                     /rpt_family="AluSx"
BASE COUNT     9122 a   9826 c  10123 g   8513 t
ORIGIN

  Query Match           12.1%;  Score 328.4;  DB 9;  Length 37584;
  Best Local Similarity   99.7%;  Pred. No. 2.2e-51;
  Matches  329;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11527 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 11468

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11467 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 11408
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Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
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Db      11407 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 11348

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11347 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 11288

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
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Db      11287 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 11228

Qy        301 GGACCGATGGGGACACTGCCTATTTTGCGG 330
              ||||||| ||||||||||||||||||||||
Db      11227 GGACCGCTGGGGACACTGCCTATTTTGCGG 11198
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RESULT 21
GGA251457
LOCUS GGA251457 509 bp mRNA linear VRT 15-FEB-2000
DEFINITION Gallus gallus partial mRNA for dopamine beta-hydroxylase.
ACCESSION AJ251457
VERSION AJ251457.1 GI:6983691
KEYWORDS dopamine beta-hydroxylase.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1
AUTHORS Ernsberger,U., Reissmann,E., Mason,I. and Rohrer,H.
TITLE The expression of dopamine beta-hydroxylase, tyrosine hydroxylase, and Phox2 transcription factors in sympathetic neurons: evidence for common regulation during noradrenergic induction and diverging regulation later in development
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 509)
AUTHORS Ernsberger,U.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1999) Ernsberger U., Ruprecht-Karls-University, Institut f. Anatomie und Zellbiologie III, Im Neuenheimer Feld 307, D-69120 Heidelberg, GERMANY
FEATURES Location/Qualifiers
source 1. .509
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/tissue_type="sympathtetic ganglia"
/dev_stage="embryonic day 8"
CDS <1. .>509
/codon_start=1
/product="dopamine beta-hydroxylase"
/protein_id="CAB75354.1"
/db_xref="GI:6983692"
/translation="HHIIMYEPVITAGNEALVHHMEIFQCTTESVNIPHYNGQCDSKM
KPEQLNYCRRVLAAWAMGAQAFYYPEEAGVAFGGPGSSRHLRLEIHYHNPLIFRGRRD
SSGIRLYYTDKLRSHDAGIMELGLVYSPLMAVPPGETAFILTGYCTDKCTQKALPEGG
IRIFASQLHT"
BASE COUNT 120 a 160 c 125 g 104 t
ORIGIN

Query Match 12.0%; Score 326.6; DB 5; Length 509;
Best Local Similarity 77.6%; Pred. No. 9.7e-51;
Matches 395; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

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Qy        720 CACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCAC 779
              |||||||| |||| ||| |||||  |  ||||   ||||||||| ||||| |||||||||
Db          1 CACCACATAATCATGTATGAGCCAGTGATCACAGCGGGCAATGAAGCCCTAGTCCACCAC 60

Qy        780 ATGGAAGTCTTCCAGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGC 839
              ||||||  |||||||||||  |  |||||   | || | ||||||| | || ||| |  ||
Db         61 ATGGAAATCTTCCAGTGCACAACCGAGTCTGTCAACATCCCCCATTACAACGGTCAATGT 120

Qy        840 GACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCC 899
              |||||||||||| || || |  |||||||||||| | |  ||||| || || ||||||
Db        121 GACTCCAAGATGAAGCCAGAGCAGCTCAACTACTGCAGGCGTGTGCTTGCAGCATGGGCC 180

Qy        900 CTGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGGG 959
              ||||  ||  |||| || |||||||| || ||||| ||  ||||||| || |||||||||
Db        181 ATGGGAGCACAGGCTTTCTACTACCCCGAAGAAGCAGGAGTTGCCTTTGGTGGTCCAGGC 240

Qy        960 TCCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACGA 1019
              |||||||| || | ||||| ||  |||||||||||| ||||||  |  |  ||| ||
Db        241 TCCTCCAGACATTTGCGCCTTGAGATTCACTACCACAATCCACTGATATTCAGAGGGCGC 300

Qy       1020 AACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGG 1079
                || ||||| || |||||| |||||||||||| ||| |||||   |  | | || ||
Db        301 CGTGATTCCTCGGGGATCCGCCTGTACTACACAGACAAACTGCGTTCCCACGATGCTGGC 360

Qy       1080 ATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCC 1139
              ||||||||||||||  |||| ||| | ||  |||||||| | || ||  ||||||| |||
Db        361 ATCATGGAGCTGGGCTTGGTCTACTCACCGCTGATGGCCGTGCCCCCGGGGGAGACTGCC 420

Qy       1140 TTCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACTGCCTCCCTCCGGG 1199
              |||||||||||||| |||||||| ||||| |||||||||  ||||||||||      |||
Db        421 TTCATCCTCACTGGGTACTGCACCGACAAATGCACCCAGAAGGCACTGCCTGAAGGTGGG 480

Qy       1200 ATCCACATCTTCGCCTCTCAGCTCCACAC 1228
              |||| |||||||||||| ||||||||||
Db        481 ATCCGCATCTTCGCCTCCCAGCTCCACAC 509
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RESULT 22
HSDBH3
LOCUS HSDBH3 276 bp DNA linear PRI 04-MAY-1990
DEFINITION Human DNA for dopamine beta-hydroxylase exon 3 (EC 1.14.17.1).
ACCESSION X13259
VERSION X13259.1 GI:30464
KEYWORDS alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 276)
AUTHORS Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation
JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
MEDLINE 89160241
PUBMED 2922261
REFERENCE 2 (bases 1 to 276)
AUTHORS Nagatsu,T.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES Location/Qualifiers
source 1. .276
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="9q34"
intron <1. .9
/note="Intron II (ca 2.3 kb)"
mRNA 10. .267
/note="Exon 3"
intron 268. .>276
/note="Intron III (ca 1.0 kb)"
BASE COUNT 59 a 86 c 81 g 50 t
ORIGIN

Query Match 9.5%; Score 258.4; DB 9; Length 276;
Best Local Similarity 99.6%; Pred. No. 5.8e-38;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        475 AAGACGGCACTGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGG 534
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 AGGACGGCACTGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGG 67

Qy        535 CCATCAACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATA 594
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Db         68 CCATCAACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATA 127

Qy        595 TCCCCGAACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCC 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 TCCCCGAACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCC 187

Qy        655 AGATCCCCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCT 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 AGATCCCCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCT 247

Qy        715 CTCGGCACCACATTATCAAG 734
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Db        248 CTCGGCACCACATTATCAAG 267
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RESULT 23
AF070919
LOCUS       AF070919                262 bp    mRNA    linear   PRI 03-SEP-1998
DEFINITION  Macaca mulatta dopamine beta-hydroxylase precursor, mRNA, partial
            cds.
ACCESSION   AF070919
VERSION     AF070919.1  GI:3220262
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 262)
  AUTHORS   Mayerhofer,A., Smith,G.D., Danilchik,M., Levine,J.E., Wolf,D.P.,
            Dissen,G.A. and Ojeda,S.R.
  TITLE     Oocytes are a source of catecholamines in the primate ovary:
            evidence for a cell-cell regulatory loop
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10990-10995 (1998)
  MEDLINE   98393758
   PUBMED   9724817
REFERENCE   2  (bases 1 to 262)
  AUTHORS   Mayerhofer,A., Smith,G.D., Danilchik,M., Levine,J.E., Wolf,D.P.,
            Dissen,G.A. and Ojeda,S.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Neuroscience, Oregon Regional Primate
            Research Center/Oregon Health Sciences University, 505 NW 185th
            Ave, Beaverton, OR 97006-3448, USA
FEATURES             Location/Qualifiers
     source          1. .262
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                     /mol_type="mRNA"
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                     /tissue_type="ovary"
     CDS             <1. .>262
                     /codon_start=2
                     /product="dopamine beta-hydroxylase precursor"
                     /protein_id="AAC33898.1"
                     /db_xref="GI:3220263"
                     /translation="DSKMKPDRLNYCRHVLAAWALGAKAFYYPEEAGIAFGGPGSSRY
                     VRLEVHYHNPLVIEGRRDSSGIRLYYTDKLRRFNAGIMELGLV"
BASE COUNT       52 a     83 c     78 g     49 t
ORIGIN

  Query Match             8.8%;  Score 239.6;  DB 9;  Length 262;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-34;
  Matches  248;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;
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Qy        839 CGACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGC 898
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Db          1 CGACTCCAAGATGAAACCTGACCGCCTCAACTACTGCCGCCACGTGCTGGCTGCCTGGGC 60

Qy        899 CCTGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGGGGTCCAGG 958
              |||||||||||||||||||||||||||||||| |||||||||||| |||||||||||| || ||
Db         61 CCTGGGTGCCAAGGCATTTTACTACCCGGAGGAAGCCGGCATTGCCTTCGGGGGCCCTGG 120

Qy        959 GTCCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATAGAAGGACG 1018
              |||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 GTCCTCCAGATACGTCCGCCTGGAAGTTCACTACCACAACCCGCTGGTGATAGAAGGACG 180

Qy       1019 AAACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGG 1078
              |||||||||||||||||||||||||||||||| |||||||||||||||| |||||
Db        181 GCGCGACTCCTCAGGCATCCGCTTGTACTACACAGACAAGCTGCGGCGCTTCAATGCGGG 240

Qy       1079 GATCATGGAGCTGGGACTGGTG 1100
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Db        241 GATCATGGAGCTGGGACTGGTG 262
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RESULT 24
DMTBHMR
LOCUS       DMTBHMR                 2894 bp    mRNA    linear   INV 27-NOV-1996
DEFINITION  D.melanogaster mRNA for tyramine-beta-hydroxylase.
ACCESSION   Z70316
VERSION     Z70316.1  GI:1296518
KEYWORDS    tyramine-beta-hydroxylase.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 2894)
  AUTHORS   Monastirioti,M., Linn,C.E. Jr. and White,K.
  TITLE     Characterization of Drosophila tyramine beta-hydroxylase gene and
            isolation of mutant flies lacking octopamine
  JOURNAL   J. Neurosci. 16 (12), 3900-3911 (1996)
  MEDLINE   96242086
   PUBMED   8656284
REFERENCE   2  (bases 1 to 2894)
  AUTHORS   Monastirioti,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-1996) Maria Monastirioti, Insect Molecular
            Genetics Group, IMBB, Foundation for Research and Technology,
            Hellas, Vasilika Vouton, Heraklion, Crete, 71110, Greece
FEATURES             Location/Qualifiers
     source          1. .2894
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                     /strain="Canton-S"
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                     /chromosome="X"
                     /clone="pDmTBH"
                     /tissue_type="head (recombinant)"
                     /clone_lib="lambda gt11 cDNA library (Salvatera)"
                     /dev_stage="adult"
     CDS             214. .2196
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                     against mammalian Dopamine-beta-hydroxylase protein
                     sequences"
                     /codon_start=1
                     /product="tyramine-beta-hydroxylase"
                     /protein_id="CAA94391.1"
                     /db_xref="GI:1296519"
                     /db_xref="FLYBASE:FBgn0010329"
                     /db_xref="SPTREMBL:Q24549"
                     /translation="MLKMPLQLSSQDGIWPARSARRLHHHHQLAYHHHKQQQQQQAKQ
                     KQKQNGVQQGRSPTFMPVMLLLLMATLLTRPLSAFSNRLSDTKLHEIYLDDKEIKLSW
                     MVDWYKQEVLFHLQNAFNEQHRWFYLGFSKRGGLADADICFFENQNGFFNAVTDTYTS
                     PDGQWVRRDYQQDCEVFKMDEFTLAFRRKFDTCDPLDLRLHEGTMYVVWARGETELAL
                     EDHQFALPNVTAPHEAGVKMLQLLRADKILIPESELDHMEITLQEAPIPSQETTYWCH
                     VQRLEGNLRRRHHIVQFEPLIRTPGIVHHMEVFHCEAGEHEEIPLYNGDCEQLPPRAK
                     ICSKVMVLWAMGAGTFTYPPEAGLPIGGPGFNPYVRLEVHFNNPEKQSGLVDNSGFRI
                     KMSKHCVSMTAVMELGLEYTDKMAIPPGQTAFPLSGYCVADCTRAALPATGIIIFGSQ
                     LHTHLRGVRVLTRHFRGEQELREVNRDDYYSNHFQEMRTLHYKPRVLPGDALVTTCYY
                     NTKDDKTALGGFSISDEMCVNYIHYYPATKLEVCKSSVSEETLENYFIYMKRTEHQHG
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                    VHLNGARSSNYRSIEWTQPRIDQLYTMYMQEPLSMQCNRSDGTRFEGRSSWEGVAATP
                    VQIRIPIHRKLCPNYNPLWLKPLEKGDCDLLGECIY"
BASE COUNT      707 a    752 c    730 g    705 t
ORIGIN

  Query Match             8.4%;  Score 228.4;  DB 3;  Length 2894;
  Best Local Similarity   53.5%;  Pred. No. 1.6e-32;
  Matches  594;  Conservative    0;  Mismatches  501;  Indels   15;  Gaps    5;

Qy        629 CATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCCAGGAGACCACGTACTGGTGCTA 688
              ||||||| ||  |   |   |     | || ||||| ||||||||||||||||||||  |
Db        981 CATGGAGATCACACTGCAGGAGGCGCCAATTCCCAGTCAGGAGACCACGTACTGGTGTCA 1040

Qy        689 CATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACATTATCAAGTACGAGCCCATCGT 748
              | || ||   ||     |||||      ||||  | |  |  ||       ||  |
Db        1041 CGTTCAGCGACTGG---AGGGCAATCTCCGGCGTCGCCATCACATCGTTCAGTTCGAGCC 1097

Qy        749 CACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCCAGTGCGCCCCCGAGAT 808
                  |  | |    || | | || || |||||||||| || || ||||   |||
Db        1098 GCTTATCCGAACGCCGGGCATCGTGCATCACATGGAAGTGTTTCACTGCGAGGCCGGTGA 1157

Qy        809 GGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAACCCGACCGCCTCAA 868
              | ||   |     | | |          | ||||||   |   |   ||    ||
Db        1158 GCACGAGGAGATTCCCCTGTATAA---CGGCGACTGTGAACAGTTGCCGCCACGGGCGAA 1214

Qy        869 CTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGGCATTTTACTACCCAGA 928
                ||||    | ||| ||| |   |||||| |||| ||      | |||  ||| ||
Db        1215 GATCTGCTCAAAAGTGATGGTCCTGTGGGCCATGGGCGCTGGCACCTTTACCTATCCTCC 1274

Qy        929 GGAAGCCGGCCTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTCCGCCTGGAAGTTCA 988
              |||||||| ||  |  |||| || || || | |     ||  | || |||||  || ||
Db        1275 GGAAGCCGGTCTACCAATCGGCGGACCCGGCTTCAATCCGTACGTTCGACTGGAGGTACA 1334

Qy        989 CTACCACAACCCACTGGTGATAGAAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTA 1048
              | | | || ||   |  |          ||        |||  ||| ||| |  ||| |   | |
Db        1335 TTTCAATAATCCGGAGAAGCAGTCGGGCTTGGTGGACAACTCCGGCTTTCGCAT---CAA 1391

Qy        1049 CACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCATGGAGCTGGGACTGGTGTACACGCC 1108
               |   | ||||   |   |   |   |||   | ||||| ||||| |||| ||||||
Db        1392 GATGTCGAAGCACTGCGTCAGTATGACGGCCGTTATGGAACTGGGCCTGGAGTACACCGA 1451

Qy        1109 AGTGATGGCCATTCCACCACGGGAGACCGCCTTCATCCTCACTGGCTACTGCACGGACAA 1168
               |||||||||||| ||  |  | ||||| |||    || |  ||||| ||   ||  |
Db        1452 CAAAATGGCCATTCCGCCTGGCCAAACCGCATTCCCGCTGAGCGGCTATTGTGTGGCGGA 1511

Qy        1169 GTGCACCCAGCTGGCACTGCCTCCCTCCGGGATCCACATCTTCGCCTCTCAGCTCCACAC 1228
               |||||  |    || |||||  |  | || |||  |||||| | |||||||| || ||
Db        1512 CTGCACACGAGCCGCTCTGCCGGCGACGGGCATCATCATCTTTGGCTCTCAGCTGCATAC 1571

Qy        1229 ACACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGAT 1288
               || |||  |||        ||  | ||     |  | || | ||  | ||||  |
Db        1572 GCATCTGCGTGGCGTTCGCGTCCTAACCCGACACTTTCGCGGCGAACAGGAGCTGCGCGA 1631

Qy        1289 CGTGAACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGTTGAAGAAGGT 1348
               |||||||  ||  | |||||      ||||||||||||||||  ||||   || | |
Db        1632 GGTGAACCGCGATGACTACTACTCGAATCACTTCCAGGAGATGCGCACCCTGCACTACAA 1691

Qy        1349 CGTGTCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACACGGAAGACCG 1408
                |   ||||  || || || |   | | ||| | |||   ||||||||  | ||
Db        1692 GCCGCGTGTCCTGCCCGGCGACGCTTTGGTAACCACTTGCTACTACAACACCAAGGA--- 1748

Qy        1409 GGAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCAACTACGTGCA 1468
               ||   | || |  | || || |||   |||   || ||||||||| |||||||| | ||
Db        1749 TGACAAGACCGCCCTCGGCGGATTCTCCATCAGCGATGAGATGTGCGTCAACTATATCCA 1808

Qy        1469 CTACTACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGCTTCCTGCA 1528
               |||||| ||    ||  | |||||| |||||||||    | ||   ||  |    ||  |
Db        1809 CTACTATCCGGCCACCAAACTGGAGGTCTGCAAGAGTTCCGTTTCCGAGGAGACGCTCGA 1868

Qy        1529 GAAGTACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTCTGCACCTGCCCTCAGGC 1588
               ||| |||||      ||| ||  |    |  | || |||   ||      |  | |
Db        1869 GAATTACTTTATTTACATGAAGCGCACGGAGCATCAGCATG---GCGTGCATTTGAATGG 1925

Qy        1589 GTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTCAACCGCGACGTACTGAA 1648
                  ||  |||     | | |       |    |||| |          |||    ||| |
Db        1926 AGCCAGGTCGTCCAATTACCGGAGCATCGAATGGACCCAGCCGCGTATCGATCAGCTGTA 1985

Qy        1649 GGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAGTCCTCAGCCGTCCGCTT 1708
                  || ||||||      | |||  |   ||||| |||||||| ||||    | |   |||||
Db        1986 CACCATGTACATGCAGGAGCCGCTGAGCATGCAGTGCAACAGGTCCGATGGCACTCGCTT 2045

Qy        1709 CCAGGGTGAATGGAACCTGCAGCCCCTGCC 1738
               | ||||    |  | |  | ||  | || |
Db        2046 CGAGGGGCGGTCTAGCTGGGAGGGCGTGGC 2075


RESULT 25
AL954801
LOCUS       AL954801               73066 bp    DNA     linear   ROD 15-NOV-2002
DEFINITION  Mouse DNA sequence from clone RP23-171K6 on chromosome 2, complete
            sequence.
ACCESSION   AL954801
VERSION     AL954801.1  GI:25137074
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 73066)
  AUTHORS   Matthews,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-171K6 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .73066
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /clone="RP23-171K6"
                     /clone_lib="RPCI-23"
BASE COUNT    18160 a  18828 c  18294 g  17784 t
ORIGIN

  Query Match             8.4%;  Score 228.4;  DB 10;  Length 73066;
  Best Local Similarity   81.3%;  Pred. No. 9.2e-33;
  Matches  265;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;
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Qy          5 TCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGC 64
              | | |||  |||||| ||  |||||||  | || ||||| || | ||||||| |||| ||
Db      16572 TTGTTGGAGCAGCCTCCCAAGCCCCAGTGTCCGTGAGGCGGCTTCCATGTACGGCACTGC 16631

Qy         65 AGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAG 124
              |||||||||||||||||||||||||||||| |||||||  |||||||  ||  |  |||||
Db      16632 TGTGGCCATCTTCCTGGTCATCCTGGTGGCTGCACTGCGGGGCTCGGAGCCTCCAGAGAG 16691

Qy        125 CCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGT 184
              |||| |||||||  |||||||||||||||||  || |||    | ||||||||||||| ||
Db      16692 CCCCTTCCCCTACCACATCCCCCTGGACCCCGAAGGGATTTTAGAGCTCTCATGGAACGT 16751

Qy        185 CAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGT 244
              ||||||   |||||||  |||||| ||||||||||  ||||   |||| | |||||| ||
Db      16752 CAGCTATGTCCAGGAGATCATCCACTTCCAGCTCCAGGTGCAAGGGCTGAGGGCTGGGGT 16811

Qy        245 CCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGAC 304
              |||||||| ||||| || || || ||| | ||||||||||||||| |  ||||||||||
Db      16812 CCTGTTTGGAATGTCAGATCGAGGAGAGATGGAGAACGCAGATCTCATCATGCTCTGGAC 16871

Qy        305 CGATGGGGACACTGCCTATTTTGCGG 330
              ||||||||||  ||||| |||||||
Db      16872 TGATGGGGACAGGGCCTACTTTGCGG 16897
```

RESULT 26
AC010965
LOCUS AC010965 186208 bp DNA linear HTG 21-NOV-2002
DEFINITION Mus musculus clone RP23-479L21, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
ACCESSION AC010965
VERSION AC010965.12 GI:25103671
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 186208)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-479L21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186208)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 186208)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:11496385.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-------------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
Center project name: L908
Center clone name: 479_L_21
--------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 176982: contig of 176982 bp in length
* 176983 177082: gap of 100 bp
* 177083 186208: contig of 9126 bp in length.
FEATURES Location/Qualifiers
source. 1. .186208
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-479L21"
/clone_lib="RPCI-23 Female Mouse BAC"
BASE COUNT 45657 a 46784 c 48095 g 45543 t 129 others
ORIGIN

Query Match 8.4%; Score 228.4; DB 2; Length 186208;
Best Local Similarity 81.3%; Pred. No. 7.9e-33;
Matches 265; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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Qy          5 TCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGC 64
              | | |||  |||||| ||  |||||||  | || ||||| || | ||||||| |||| ||
Db     125723 TTGTTGGAGCAGCCTCCCAAGCCCCAGTGTCCGTGAGGCGGCTTCCATGTACGGCACTGC 125782

Qy         65 AGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAG 124
              |||||||||||||||||||||||||||||| |||||||  |||||||  ||  |  |||||
Db     125783 TGTGGCCATCTTCCTGGTCATCCTGGTGGCTGCACTGCGGGGCTCGGAGCCTCCAGAGAG 125842

Qy        125 CCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGT 184
              |||| |||||||  |||||||||||||||||  || |||    | ||||||||||||| ||
Db     125843 CCCCTTCCCCTACCACATCCCCCTGGACCCCGAAGGGATTTTAGAGCTCTCATGGAACGT 125902

Qy        185 CAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGT 244
              ||||||   |||||||  |||||| ||||||||||  ||||   |||| | |||||| ||
Db     125903 CAGCTATGTCCAGGAGATCATCCACTTCCAGCTCCAGGTGCAAGGGCTGAGGGCTGGGGT 125962

Qy        245 CCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGAC 304
              |||||||| ||||| || || || ||| | ||||||||||||||| |  ||||||||||
Db     125963 CCTGTTTGGAATGTCAGATCGAGGAGAGATGGAGAACGCAGATCTCATCATGCTCTGGAC 126022

Qy        305 CGATGGGGACACTGCCTATTTTGCGG 330
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Db     126023 TGATGGGGACAGGGCCTACTTTGCGG 126048
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RESULT 27
AC091762/c
LOCUS       AC091762               205420 bp    DNA     linear   HTG 11-JUN-2003
DEFINITION  Mus musculus clone rp23-151n4 map 2 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 2 ordered pieces.
ACCESSION   AC091762
VERSION     AC091762.26  GI:31581643
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 205420)
  AUTHORS   Jiang,X., Song,L. and Roe,B.A.
  TITLE     Mus musculus Chromosome 10 BAC Clone rp23-151n4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 205420)
  AUTHORS   Jiang,X., Song,L. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3  (bases 1 to 205420)
  AUTHORS   Jiang,X., Song,L. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Jun 11, 2003 this sequence version replaced gi:31560185.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1    21604: contig of 21604 bp in length
            *   21605    21704: gap of unknown length
            *   21705   205420: contig of 183716 bp in length.
FEATURES             Location/Qualifiers
     source          1. .205420
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /map="2"
                     /clone="rp23-151n4"
                     /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
BASE COUNT    51372 a  53298 c  51045 g  49605 t    100 others
ORIGIN

  Query Match             8.4%;  Score 228.4;  DB 2;  Length 205420;
  Best Local Similarity   81.3%;  Pred. No. 7.8e-33;
  Matches  265;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          5 TCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGC 64
              | | |||  |||||| ||  |||||||  | || ||||| || | ||||||| |||| ||
Db      59419 TTGTTGGAGCAGCCTCCCAAGCCCCAGTGTCCGTGAGGCGGCTTCCATGTACGGCACTGC 59360

Qy         65 AGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAG 124
              |||||||||||||||||||||||||||||| ||||||| ||||||||  || |  |||||
Db      59359 TGTGGCCATCTTCCTGGTCATCCTGGTGGCTGCACTGCGGGGCTCGGAGCCTCCAGAGAG 59300

Qy        125 CCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGT 184
              |||| ||||||| |||||||||||||||||| || |||    | ||||||||||||| ||
Db      59299 CCCCTTCCCCTACCACATCCCCCTGGACCCCGAAGGGATTTTAGAGCTCTCATGGAACGT 59240

Qy        185 CAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGT 244
              ||||||   ||||||| |||||| |||||||||| |||||   |||| | |||||| ||
Db      59239 CAGCTATGTCCAGGAGATCATCCACTTCCAGCTCCAGGTGCAAGGGCTGAGGGCTGGGGT 59180

Qy        245 CCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGAC 304
              ||||||||| ||||| || || || ||| | |||||||||||||||| |  ||||||||||
Db      59179 CCTGTTTGGAATGTCAGATCGAGGAGAGATGGAGAACGCAGATCTCATCATGCTCTGGAC 59120

Qy        305 CGATGGGGACACTGCCTATTTTGCGG 330
              ||||||||||  ||||| |||||||
Db      59119 TGATGGGGACAGGGCCTACTTTGCGG 59094


RESULT 28
AF075385
LOCUS       AF075385                 663 bp    mRNA    linear   VRT 17-JUN-1999
DEFINITION  Danio rerio dopamine beta hydroxylase precursor (dbh) mRNA, partial
            cds.
ACCESSION   AF075385
VERSION     AF075385.1  GI:4959064
KEYWORDS    .
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Guo,S., Wilson,S.W., Cooke,S., Chitnis,A.B., Driever,W. and
            Rosenthal,A.
  TITLE     Mutations in the zebrafish unmask shared regulatory pathways
            controlling the development of catecholaminergic neurons
  JOURNAL   Dev. Biol. 208 (2), 473-487 (1999)
  MEDLINE   99208650
   PUBMED   10191060
REFERENCE   2  (bases 1 to 663)
  AUTHORS   Guo,S. and Rosenthal,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-1998) Neuroscience, Genentech Inc., 1 DNA Way,
            South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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                     /product="dopamine beta hydroxylase precursor"
                     /protein_id="AAD34219.1"
                     /db_xref="GI:4959065"
                     /translation="GPCDWKMKPRNLNYCRHVLAAWAMGAEPFYYPADAGLPMGGEGS
                     SRFLRLEVHYHNPLLLSGRRDSSGIRLWYSPSLRRFDAGIMELGLVYTPVMAIPPRQR
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                     SSTHYQIIRVLHKMVTGLPXRCSAHXVADSNTRGTXXKVYCGXGFGNYGGKMCRQXNV
                     PKA"
BASE COUNT      144 a    165 c    180 g    165 t      9 others
ORIGIN

  Query Match             8.1%;  Score 221.6;  DB 5;  Length 663;
  Best Local Similarity   66.6%;  Pred. No. 3.7e-31;
  Matches  359;  Conservative    0;  Mismatches  177;  Indels    3;  Gaps    3;

Qy        831 GGGCCCTGCGACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCC 890
              ||||| || || |  |||||||| ||    |   || || || ||| | || || |||||
Db          1 GGGCCGTGTGATTGGAAGATGAAGCCGCGCAATCTTAATTATTGCAGACATGTTCTGGCT 60

Qy        891 GCCTGGGCCCTGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGCCTTGCCTTCGGG 950
              ||||||||| |||| ||  || |||| ||||| || |  || || ||  |  |  | ||
Db         61 GCCTGGGCCATGGGAGCAGAGCCATTCTACTATCCTGCTGACGCTGGTTTGCCTATGGGA 120
```

```
Qy        951 GGTCCAGGGTCCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAACCCACTGGTGATA 1010
              ||   ||| || || || | ||| || || |||||||| |||||||||| ||  |  ||
Db        121 GGAGAAGGATCTTCTAGGTTTCTTCGTCTTGAAGTTCATTACCACAACCCTCTCCTTTTA 180

Qy       1011 GAAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTC 1070
              ||| || |  |||||||| ||||| || || |  ||||    |     |||||| | ||
Db        181 TCAGGGCGGAGGGACTCCTCGGGCATTCGTTTATGGTACAGTCCATCTCTGCGGAGGTTT 240

Qy       1071 AACGCGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGG 1130
              |||| || |||||||||| || ||||| |||||  || |||||||||||||| || ||
Db        241 GACGCAGGCATCATGGAGCTTGGGCTGGTCTACACTCCTGTGATGGCCATTCCCCCCCGC 300

Qy       1131 GAGACCGCCTTCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACTGCCT 1190
              ||  | | |||   |||||||| |||||||| | ||| ||||| |||  ||| || ||
Db        301 CAGCGCTCTTTCCAGCTCACTGGATACTGCACCGCCAAATGCACACAGACGGCTCTTCCA 360

Qy       1191 CCCTCCGGG-ATCCACATCTTCGCCTCTCAGCTCCACACACACCTGACTGGGAGAAAGGT 1249
              ||| || |||||||| ||||| ||||| |||||·|| ||| | ||       |||
Db        361 AGTAGGGGGCATACACATCTTTGCCTCCCAGCTGCACACTCATCTGGCCGGTCTTGGGGT 420

Qy       1250 GGTCACAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTG-AACCAGGACAATCACT 1308
              || ||  |||| || |  || |  ||   | || | ||| ||  ||||||  || |
Db        421 CAGGACTGTCTTGGTGCGAGGAGGTCAAGANGTGNAGGTGGTGCAAGGAGGACAGACATT 480

Qy       1309 AC-AGCCCTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTCGTGTCGGTCCATCCGGG 1366
              | ||| | || | ||||   |||||  | ||  | ||| | ||| | |  |  ||  |
Db        481 TCAAGCACACATTACCAGATCATCCGTGTTTTACATAAGATGGTGACTGGTCTGCCANG 539
```

RESULT 29
AC126203
LOCUS AC126203 225079 bp DNA linear HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-177E3, WORKING DRAFT SEQUENCE, 2 unordered pieces.
ACCESSION AC126203
VERSION AC126203.3 GI:25007867
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 225079)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 225079)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 225079)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 15, 2002 this sequence version replaced gi:23196254.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
-------------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-------------- Project Information
Center project name: GZGS
Center clone name: CH230-177E3
-------------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 191488 bases at least Q40
Consensus quality: 194511 bases at least Q30
Consensus quality: 196425 bases at least Q20
Estimated insert size: 199941; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 223772: contig of 223772 bp in length

```
            *   223773   223872: gap of unknown length
            *   223873   225079: contig of 1207 bp in length.
FEATURES             Location/Qualifiers
     source          1. .225079
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-177E3"
     misc_feature    1. .1686
                     /note="wgs_contig"
BASE COUNT    46863 a  51393 c  52190 g  47818 t  26815 others
ORIGIN

  Query Match             8.1%;  Score 220;  DB 2;  Length 225079;
  Best Local Similarity   81.0%;  Pred. No. 2.8e-31;
  Matches  256;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy         15 AGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCACAGCAGTGGCCATC 74
              ||||| ||| |||||||| | || ||||| || | |||||| |||| || |||||||||
Db     165644 AGCCTCCCCAGCCCCAGCGTCCGTGAGGCGGCTTCCATGTATGGCACTGCTGTGGCCATC 165703

Qy         75 TTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCCCCCTCCCC 134
              |||||||||||||||||||| ||||||||||||||||  || |  ||||||||| ||||
Db     165704 TTCCTGGTCATCCTGGTGGCTGCACTGCAGGGCTCGGAGCCTCCGGAGAGCCCCTTCCCT 165763

Qy        135 TATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCAGCTACACC 194
              || |||||||||||||||||| || ||| |  | |||||||| ||||| ||||||||   |
Db     165764 TACCACATCCCCCTGGACCCTGAAGGGACTTTAGAGCTCTCGTGGAACGTCAGCTATGAC 165823

Qy        195 CAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCCTGTTTGGG 254
              ||||||  |||||| |||||||||| |||||   |||  | |||||| |||||||| ||
Db     165824 CAGGAGATCATCCACTTCCAGCTCCAGGTGCAAGGGCCGAGGGCTGGGGTCCTGTTCGGA 165883

Qy        255 ATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCGATGGGGAC 314
              ||||| || || || ||| | |||||||||| |||||  |||||||||| || ||||||
Db     165884 ATGTCGGATCGAGGTGAGATGGAGAACGCAGACCTCGTCATGCTCTGGACTGACGGGGAC 165943

Qy        315 ACTGCCTATTTTGCGG 330
              |   |||| |||||||
Db     165944 AGGACCTACTTTGCGG 165959


RESULT 30
AX347199/c
LOCUS       AX347199               2037 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 2270 from Patent WO0200928.
ACCESSION   AX347199
VERSION     AX347199.1  GI:18495087
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 2270 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .2037
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT      417 a     49 c    558 g   1013 t
ORIGIN

  Query Match             7.1%;  Score 193;  DB 6;  Length 2037;
  Best Local Similarity   74.2%;  Pred. No. 6.7e-26;
  Matches  244;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              ||| |||||   ||| ||| |||| ||||| ||| ||  |  || ||||||| |||| ||
Db        338 TCAATCGCTAAACCAACCTACCCGACCCCAACATACGAAAAACAACCTTCATATACAACA 279

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
              || || |  |||||||||  |||||||  |  ||||||| ||    |||| ||||||||
Db        278 CAACAATAACCATCTTCCTAATCATCCTAATAACCGCACTACAAAACTCGACTCCCCGTA 219

Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
              | | ||||||||||||||||||||||||  ||||| |   |||||  | |||||||  |
Db        218 AAAACCCCCTCCCCTATCACATCCCCCTAAACCCGAAAAAATCCCTAAAACTCTCATAAA 159

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240
              || ||| |||||||||  |  ||||||||||||| |||||  | || |  |||||  ||
Db        158 ATATCAACTACACCCAAAAAACCATCCATTTCCAACTCCTAATACGAAAACTCAAAACTA 99

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
              |||||| |||   || |||||||||  ||| |||| | |||||| |||||||  | ||||
Db         98 ACGTCCTATTTAAAATATCCGACCGTAACGAACTTAAAAACGCAAATCTCGTAATACTCT 39

Qy        301 GGACCGATGGGGACACTGCCTATTTTGCG 329
              ||||||    ||||| |||||||| ||
Db         38 AAACCGATAAAAACACTACCTATTTTACG 10


RESULT 31
AX348532/c
LOCUS       AX348532               2037 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 40 from Patent WO0202809.
ACCESSION   AX348532
VERSION     AX348532.1  GI:18614567
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of behavioural disorders, neurological disorders and
            cancer
  JOURNAL   Patent: WO 0202809-A 40 10-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .2037
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT      417 a     49 c    558 g   1013 t
ORIGIN

  Query Match             7.1%;  Score 193;  DB 6;  Length 2037;
  Best Local Similarity   74.2%;  Pred. No. 6.7e-26;
  Matches  244;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              ||| |||||   ||| ||| |||| ||||| ||| ||  |  || ||||||| |||| ||
Db        338 TCAATCGCTAAACCAACCTACCCGACCCCAACATACGAAAAACAACCTTCATATACAACA 279

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
              || || |  |||||||||  |||||||  |  ||||||| ||    |||| ||||||||
Db        278 CAACAATAACCATCTTCCTAATCATCCTAATAACCGCACTACAAAACTCGACTCCCCGTA 219

Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
              | | ||||||||||||||||||||||||  ||||| |   |||||  | |||||||  |
Db        218 AAAACCCCCTCCCCTATCACATCCCCCTAAACCCGAAAAAATCCCTAAAACTCTCATAAA 159

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240
              || ||| |||||||||  |  ||||||||||||| |||||  | || |  |||||  ||
Db        158 ATATCAACTACACCCAAAAAACCATCCATTTCCAACTCCTAATACGAAAACTCAAAACTA 99

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
              |||||| |||   || |||||||||  ||| |||| | |||||| |||||||  | ||||
Db         98 ACGTCCTATTTAAAATATCCGACCGTAACGAACTTAAAAACGCAAATCTCGTAATACTCT 39

Qy        301 GGACCGATGGGGACACTGCCTATTTTGCG 329
              ||||||    ||||| |||||||| ||
```

```
Db         38 AAACCGATAAAAACACTACCTATTTTACG 10


RESULT 32
HSDBH4
LOCUS       HSDBH4                     195 bp    DNA     linear   PRI 04-MAY-1990
DEFINITION  Human DNA for dopamine beta-hydroxylase exon 4 (EC 1.14.17.1).
ACCESSION   X13260
VERSION     X13260.1  GI:30465
KEYWORDS    alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 195)
  AUTHORS   Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
  TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
            different 3'-terminal regions are produced through alternative
            polyadenylation
  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 195)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES             Location/Qualifiers
     source          1. .195
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="9q34"
     intron          <1. .9
                     /note="Intron III (ca 1.0 kb)"
     mRNA            10. .186
                     /note="Exon 4"
     intron          187. .>195
                     /note="Intron IV (ca 0.8 kb)"
BASE COUNT       37 a     75 c     52 g     31 t
ORIGIN

  Query Match             6.6%;  Score 180;  DB 9;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches  180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        733 AGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCC 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 AGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAGTCTTCC 67

Qy        793 AGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGA 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 AGTGCGCCCCCGAGATGGACAGCGTCCCCCACTTCAGCGGGCCCTGCGACTCCAAGATGA 127

Qy        853 AACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGG 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGG 187


RESULT 33
AX347198
LOCUS       AX347198                2037 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 2269 from Patent WO0200928.
ACCESSION   AX347198
VERSION     AX347198.1  GI:18495086
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 2269 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .2037
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT       417 a     49 c    645 g    926 t
ORIGIN

  Query Match             6.6%;  Score 179.6;  DB 6;  Length 2037;
  Best Local Similarity   71.5%;  Pred. No. 2.1e-23;
  Matches  236;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              | ||||| |||| || || ||| || |||||||||| || || ||||| || |
Db       1700 TTAGTCGTTGGGTTAGTTTGTTCGGTTTTAGTATGCGGGAGGTAGTTTTTATGTATAGTA 1759

Qy         61 CAGCAGTGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTG 120
              || ||||| || ||  |||| ||  |||||| || | || |||| |||| |    ||||
Db       1760 TAGTAGTGGTTATTTTTTTGGTTATTTTGGTGGTCGTATTGTAGGGTTCGGTTTTTCGTG 1819

Qy        121 AGAGCCCCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
              ||||    |   ||| | ||   |||| |||||||||   ||||| | | |||||
Db       1820 AGAGTTTTTTTTTTATTATATTTTTTTGGATTCGGAGGGGTTTTTGGAGTTTTTATGGA 1879

Qy        181 ATGTCAGCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTG 240
              |||| || || |   |||||  ||  ||||  || |  |||||||||| | |||| ||
Db       1880 ATGTTAGTTATATTTAGGAGGTTATTTATTTTTAGTTTTTGGTGCGGAGGTTTAAGGTTG 1939

Qy        241 GCGTCCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCT 300
              ||||  |||||||||||| ||| |||||||| |||||||| |||| |||||||| | |
Db       1940 GCGTTTTGTTTGGGATGTTCGATCGTGGCGAGTTTGAGAACGTAGATTTCGTGGTGTTTT 1999

Qy        301 GGACCGATGGGGACACTGCCTATTTTGCGG 330
              ||| |||||||||  | ||  ||||||||||
Db       2000 GGATCGATGGGGATATTGTTTATTTTGCGG 2029


RESULT 34
AX348531
LOCUS       AX348531                2037 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 39 from Patent WO0202809.
ACCESSION   AX348531
VERSION     AX348531.1  GI:18614566
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of behavioural disorders, neurological disorders and
            cancer
  JOURNAL   Patent: WO 0202809-A 39 10-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .2037
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT       417 a     49 c    645 g    926 t
ORIGIN

  Query Match             6.6%;  Score 179.6;  DB 6;  Length 2037;
  Best Local Similarity   71.5%;  Pred. No. 2.1e-23;
  Matches  236;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy          1 TCAGTCGCTGGGCCAGCCTGCCCGGCCCCAGCATGCGGGAGGCAGCCTTCATGTACAGCA 60
              | ||||| |||| || || ||| || |||||||||| || || ||||| || |
Db       1700 TTAGTCGTTGGGTTAGTTTGTTCGGTTTTAGTATGCGGGAGGTAGTTTTTATGTATAGTA 1759
```

RESULT 35
BC037684
LOCUS BC037684 2164 bp mRNA linear ROD 27-SEP-2002
DEFINITION Mus musculus, RIKEN cDNA 3230402N08 gene, clone IMAGE:3675929, mRNA.
ACCESSION BC037684
VERSION BC037684.1 GI:23337062
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2164)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 80 Row: d Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10946925.

FEATURES Location/Qualifiers
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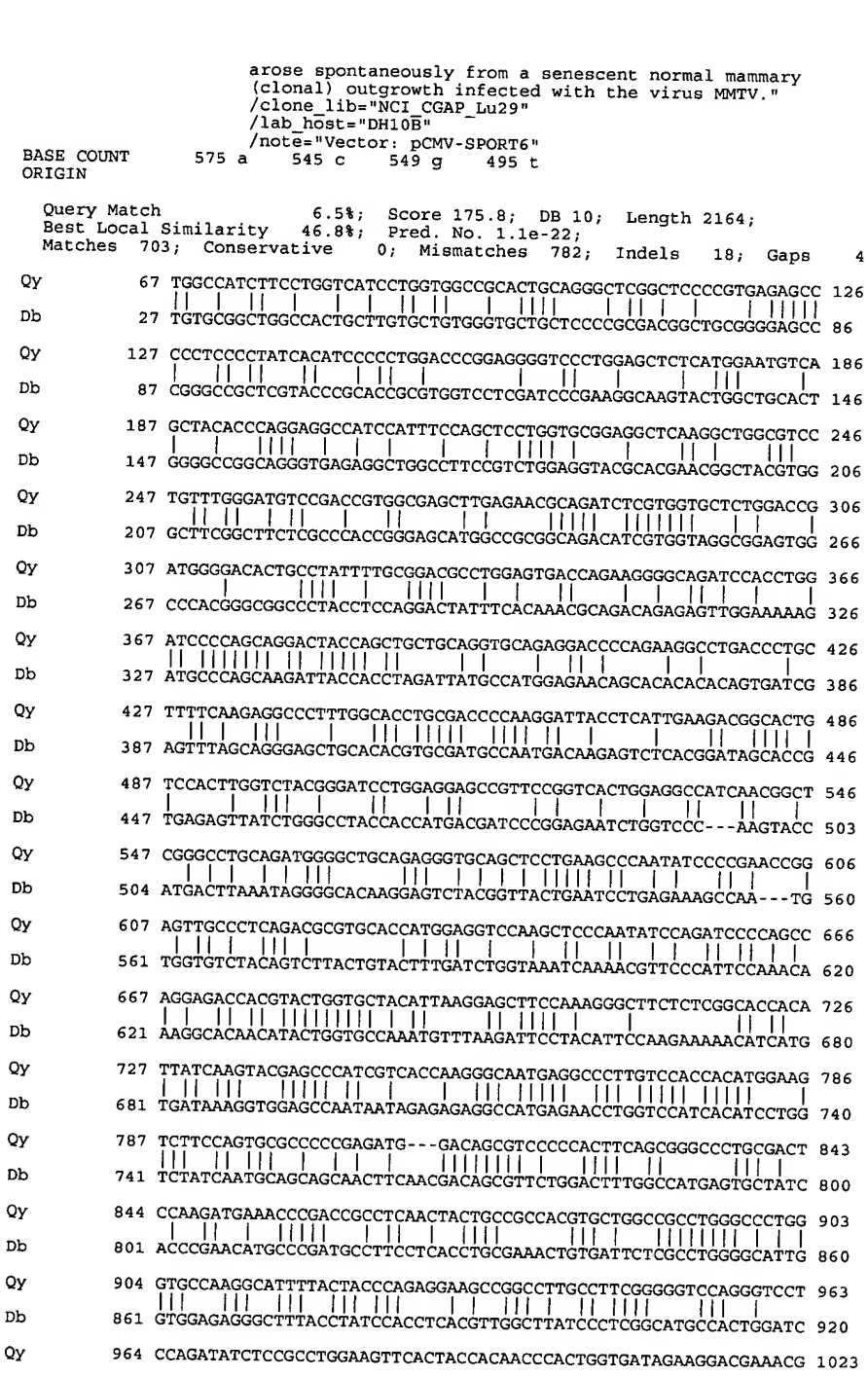
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3675929"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
/clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
BASE COUNT 575 a 545 c 549 g 495 t
ORIGIN

Query Match 6.5%; Score 175.8; DB 10; Length 2164;
Best Local Similarity 46.8%; Pred. No. 1.1e-22;
Matches 703; Conservative 0; Mismatches 782; Indels 18; Gaps 4;



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Db        921 CTCGTTATGTGCTTTTAGAGGTCCACTACGATAATCCCGCACGGAGGAAAGGCTTAATAG 980

Qy       1024 ACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCA 1083

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Qy       1084 TGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCA 1143

Db       1041 TTGAGGCTGGCCTCTGGGTGAGCCTCTTCCACACAATTCCCCCAGGGATGCCCGAGTTCC 1100

Qy       1144 TCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACT---------GCCTCCCT 1194

Db       1101 ATTCTGAGGGTCACTGCACTCTGGAGTGCCTAGAGGAGGCCCTGGGAGCTGAGAAACCAA 1160

Qy       1195 CCGGGATCCACATCTTCGCCTCTCAGCTCCACACACACCTGACTGGGAGAAAGGTGGTCA 1254

Db       1161 GTGGAATCCACGTGTTTGCGGTCCTTCTCCATGCTCACCTGGCAGGCAAAGGCATCAGGC 1220

Qy       1255 CAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTGAACCAGGACAATCACTACAGCC 1314

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Qy       1315 CTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGC 1374

Db       1281 TTAATTTCCAGGAGTTTCAGTATCTGAGGGAAGAACAAACAATCTTACCAGGTGATAACC 1340

Qy       1375 TCATCACCTCCTGCACGTACAACACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCG 1434

Db       1341 TGATCACTGAATGCCGGTATAACACCAAGGACCGAGCTGTGATGACTTGGGGAGGACTAA 1400

Qy       1435 GGATCCTGGAGGAGATGTGTGTCAACTACGTGCACTACTACCCCCAGACGCAGCTGGAGC 1494

Db       1401 GCACCAGGAATGAAATGTGTCTCTCATACCTTCTTTATTATCCAAGAGTTAACCTGACCC 1460

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Qy       1555 TCA 1557

Db       1521 ACA 1523
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RESULT 36
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LOCUS AB041606 2903 bp mRNA linear ROD 30-JUN-2000
DEFINITION Mus musculus brain cDNA; clone MNCb-5203.
ACCESSION AB041606
VERSION AB041606.1 GI:7670475
KEYWORDS fis (full insert sequence).
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and Hashimoto,K.
TITLE isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2903)
AUTHORS Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT URL: http://www.nih.go.jp/yoken/genebank/
Lib Name: Sugano mouse brain mncb
Lab host: TOP10
Vector: pME18S-FL3
1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb.The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al.(University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAAGCTGCG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).
A part of this sequence is reported in AU080082.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-5203"
/sex="female"
/clone_lib="Sugano mouse brain mncb"
/dev_stage="adult"
CDS 23. .1864
/note="unnamed protein product"
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BASE COUNT 748 a 710 c 710 g 735 t
ORIGIN

Query Match 6.4%; Score 174.2; DB 10; Length 2903;
Best Local Similarity 46.7%; Pred. No. 2e-22;
Matches 702; Conservative 0; Mismatches 783; Indels 18; Gaps 4;

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Qy         67 TGGCCATCTTCCTGGTCATCCTGGTGGCCGCACTGCAGGGCTCGGCTCCCCGTGAGAGCC 126

Db         24 TGTGCGGCTGGCCACTGCTTGTGCTGTGGGCGCTGCTCCCCGCGACGGCTGCGGGAAGCC 83

Qy        127 CCCTCCCCTATCACATCCCCCTGGACCCGGAGGGGTCCCTGGAGCTCTCATGGAATGTCA 186

Db         84 CGGGCCGCTCGTACCCGCACCGCGTGGTCCTCGATCCCGAAGGCAAGTACTGGCTGCACT 143

Qy        187 GCTACACCCAGGAGGCCATCCATTTCCAGCTCCTGGTGCGGAGGCTCAAGGCTGGCGTCC 246

Db        144 GGGGCCGGCAGGGCGAGAGGCTGGCCTTCCGTCTGGAGGTACGCACGAACGGCTACGTGG 203

Qy        247 TGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCAGATCTCGTGGTGCTCTGGACCG 306

Db        204 GCTTCGGCTTCTCGCCCACCGGGAGCATGGCCGCGGCAGACATCGTGGTAGGCGGAGTGG 263

Qy        307 ATGGGGACACTGCCTATTTTGCGGACGCCTGGAGTGACCAGAAGGGGCAGATCCACCTGG 366

Db        264 CCCACGGGCGGCCCTACCTCCAGGACTATTTCACAAACGCAGACAGAGAGTTGGAAAAAG 323

Qy        367 ATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAGAGGACCCCAGAAGGCCTGACCCTGC 426

Db        324 ATGCCCAGCAAGATTACCACCTAGATTACGCCATGGAGAACAGCACACACACAGTGATCG 383

Qy        427 TTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAGGATTACCTCATTGAAGACGGCACTG 486

Db        384 AGTTTAGCAGGGAGCTGCACACGTGCGATGTCAATGTCAAGAGTCTCACGGATAGCACCG 443
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Qy        487 TCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCT 546
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Qy        547 CGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTCCTGAAGCCCAATATCCCCGAACCGG 606
Db        501 ATGACTTAAATAGGGGCACAAGGAGTCTACGGTTACTGAATCCTGAGAAAGCCAATGTGG 560

Qy        607 AGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGCTCCCAATATCCAGATCCCCAGCC 666
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Qy        667 AGGAGACCACGTACTGGTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGCACCACA 726
Db        618 AAGGCACAACATACTGGTGCCAAATGTTTAAGATTCCTACATTCCAAGAAAAACATCATG 677

Qy        727 TTATCAAGTACGAGCCCATCGTCACCAAGGGCAATGAGGCCCTTGTCCACCACATGGAAG 786
Db        678 TGATAAAGGTGGAGCCAATAATAGAGAGAGGCCATGAGAACCTGGTCCATCACATCCTGG 737

Qy        787 TCTTCCAGTGCGCCCCCGAGATG---GACAGCGTCCCCCACTTCAGCGGGCCCTGCGACT 843
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Qy        844 CCAAGATGAAACCCGACCGCCTCAACTACTGCCGCCACGTGCTGGCCGCCTGGGCCCTGG 903
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Qy       1024 ACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAACGCGGGGATCA 1083
Db        978 ACAGTTCGGGGCTGAGGGTTTTCCATACTACAGATATAAGGAGATATGACGCAGGGGTGA 1037

Qy       1084 TGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGAGACCGCCTTCA 1143
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Qy       1144 TCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGGCACT---------GCCTCCCT 1194
Db       1098 ATTCTGAGGGTCACTGCACTCTGGAGTGCCTAGAGGAGGCCCTGGGAGCTGAGAAACCAA 1157

Qy       1195 CCGGGATCCACATCTTCGCCTCTCAGCTCCACACACACCTGACTGGGAGAAAGGTGGTCA 1254
Db       1158 GTGGAATCCACGTGTTTGCGGTCCTTCTCCATGCTCACCTGGCAGGCAAAGGCATCAGGC 1217

Qy       1255 CAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTGAACCAGGACAATCACTACAGCC 1314
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Qy       1315 CTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTCGTGTCGGTCCATCCGGGAGATGTGC 1374
Db       1278 TTAATTTCCAGGAGTTTCAGTATCTGAGGGAAGAACAAACAATCTTACCAGGTGATAACC 1337

Qy       1375 TCATCACCTCCTGCACGTACAACACGGAAGACCGGGAGCTGGCCACAGTGGGGGGCTTCG 1434
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Qy       1435 GGATCCTGGAGGAGATGTGTGTCAACTACGTGCACTACTACCCCCAGACGCAGCTGGAGC 1494
Db       1398 GCACCAGGAATGAAATGTGTCTCTCATACCTTCTTTATTATCCAAGAGTTAACCTGACCC 1457

Qy       1495 TCTGCAAGACGGCTGTGGACGCCGGCTTCCTGCAGAAGTACTTCCACCTCATCAACAGGT 1554
Db       1458 GGTGCTCCAGCATCCCAGACATCATGGAACAGCTGCAGTTCATCGGCGTGAAGGAGATCT 1517

Qy       1555 TCA 1557
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Db       1518 ACA 1520
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RESULT 37
BC025892

LOCUS	BC025892 2796 bp mRNA linear ROD 16-APR-2003
DEFINITION	Mus musculus RIKEN cDNA 3230402N08 gene, mRNA (cDNA clone IMAGE:5038657), partial cds.
ACCESSION	BC025892
VERSION	BC025892.1 GI:19483984
KEYWORDS	.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 2796)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 2796)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: j Column: 21.
FEATURES	Location/Qualifiers
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                     (clonal) outgrowth infected with the virus MMTV."
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     CDS             <1. .1627
                     /gene="3230402N08Rik"
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                     HTIPPGMPEFHSEGHCTLECLEEALGAEKPSGIHVFAVLLHAHLAGKGIRLRHFRKGE
                     EMKLLAYDDDYDFNFQEFQYLREEQTILPGDNLITECRYNTKDRAVMTWGGLSTRNEM
                     CLSYLLYYPRVNLTRCSSIPDIMEQLQFIGVKEIYRPVTTWPFIIKSPKQYRNLSFMD
                     AMNKFKWTKKEGLSFNKLVLSLPVNVRCSKTDNAEWSIQGMTAIPPDIKRPYEAEPLV
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BASE COUNT      759 a    657 c    630 g    750 t
ORIGIN

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  Best Local Similarity  48.1%;  Pred. No. 5.3e-22;
  Matches  620;  Conservative    0;  Mismatches  650;  Indels   18;  Gaps    4;

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Db          2 GCAGACATCGTGGTAGGCGGAGTGGCCCACGGGCGGCCCTACCTCCAGGACTATTTCACA 61

Qy        342 GACCAGAAGGGGCAGATCCACCTGGATCCCCAGCAGGACTACCAGCTGCTGCAGGTGCAG 401
              ||     |  || | |    ||| ||||||| || ||||| ||     | |    |
Db         62 AACGCAGACAGAGAGTTGGAAAAAGATGCCCAGCAAGATTACCACCTAGATTATGCCATG 121

Qy        402 AGGACCCCAGAAGGCCTGACCCTGCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCAAG 461
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Db        122 GAGAACAGCACACACACAGTGATCGAGTTTAGCAGGGAGCTGCACACGTGCGATGCCAAT 181

Qy        462 GATTACCTCATTGAAGACGGCACTGTCCACTTGGTCTACGGGATCCTGGAGGAGCCGTTC 521
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Db        182 GACAAGAGTCTCACGGATAGCACCGTGAGAGTTATCTGGGCCTACCACCATGACGATCCC 241

Qy        522 CGGTCACTGGAGGCCATCAACGGCTCGGGCCTGCAGATGGGGCTGCAGAGGGTGCAGCTC 581
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Qy        582 CTGAAGCCCAATATCCCCGAACCGGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAA 641
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Db        299 CTGAATCCTGAGAAAGCCAA---TGTGGTGTCTACAGTCTTACTGTACTTTGATCTGGTA 355

Qy        642 GCTCCCAATATCCAGATCCCCAGCCAGGAGACCACGTACTGGTGCTACATTAAGGAGCTT 701
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Qy        702 CCAAAGGGCTTCTCTCGGCACCACATTATCAAGTACGAGCCCATCGTCACCAAGGGCAAT 761
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Qy        762 GAGGCCCTTGTCCACCACATGGAAGTCTTCCAGTGCGCCCCCGA---GATGGACAGCGTC 818
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Qy        819 CCCCACTTCAGCGGGCCCTGCGACTCCAAGATGAAACCCGACCGCCTCAACTACTGCCGC 878
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Db        536 CTGGACTTTGGCCATGAGTGCTATCACCCGAACATGCCCGATGCCTTCCTCACCTGCGAA 595

Qy        879 CACGTGCTGGCCGCCTGGGCCCTGGGTGCCAAGGCATTTTACTACCCAGAGGAAGCCGGC 938
              |||  |   |||||||| | | ||||   |||  |||  ||| |||     | |  |||
Db        596 ACTGTGATTCTCGCCTGGGGCATTGGTGGAGAGGGCTTTACCTATCCACCTCACGTTGGC 655

Qy        939 CTTGCCTTCGGGGGTCCAGGGTCCTCCAGATATCTCCGCCTGGAAGTTCACTACCACAAC 998
              |  || ||||    |||  |    |  | ||| | |   | || || ||||||  | ||
Db        656 TTATCCCTCGGCATGCCACTGGATCCTCGTTATGTGCTTTTAGAGGTCCACTACGATAAT 715

Qy        999 CCACTGGTGATAGAAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAG 1058
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Db        716 CCCGCACGGAGGAAAGGCTTAATAGACAGTTCGGGGCTGAGGGTTTTCCATACTACAGAT 775

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              |  || | |  |||| ||  | ||| ||  || ||   |  |  |  |  |  |
Db        776 ATAAGGAGATATGACGCAGGAGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCACACA 835

Qy       1119 ATTCCACCACGGGAGACCGCCTTCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAG 1178
              ||||| ||| ||  | |||  |||           ||  |||||||     |||||   ||
Db        836 ATTCCCCCAGGGATGCCCGAGTTCCATTCTGAGGGTCACTGCACTCTGGAGTGCCTAGAG 895

Qy       1179 CTGGCACTGCCT---------CCCTCCGGGATCCACATCTTCGCCTCTCAGCTCCACACA 1229
              |||  |||          ||    || ||||||  | ||  ||     |  |||||  |
Db        896 GAGGCCCTGGGAGCTGAGAAACCAAGTGGAATCCACGTGTTTGCGGTCCTTCTCCATGCT 955

Qy       1230 CACCTGACTGGGAGAAAGGTGGTCACAGTGCTGGTCCGGGACGGCCGGGAGTGGGAGATC 1289
              ||||||  | ||  | |  |           |  | ||  |  ||   |  | | |
Db        956 CACCTGGCAGGCAAAGGCATCAGGCTGCGTCATTTTCGAAAAGGAGAGGAAATGAAGTTG 1015

Qy       1290 GTGAACCAGGACAATCACTACAGCCCTCACTTCCAGGAGATCCGCATGTTGAAGAAGGTC 1349
              ||    | ||  |  | ||   |  | |  |||||||| | |      ||| | | |
Db       1016 CTGGCTTATGATGACGATTATGACTTTAATTTCCAGGAGTTTCAGTATCTGAGGGAAGAA 1075

Qy       1350 GTGTCGGTCCATCCGGGAGATGTGCTCATCACCTCCTGCACGTACAACACGGAAGACCGG 1409
              |  ||   || || |||   || |||||     |||  ||| |||||  | |||||
Db       1076 CAAACAATCTTACCAGGTGATAACCTGATCACTGAATGCCGGTATAACACCAAGGACCGA 1135

Qy       1410 GAGCTGGCCACAGTGGGGGGCTTCGGGATCCTGGAGGAGATGTGTGTCAACTACGTGCAC 1469
              |  ||   ||  ||| ||  |  | | |  | | || |||||| ||   ||| | |
Db       1136 GCTGTGATGACTTGGGGAGGACTAAGCACCAGGAATGAAATGTGTCTCTCATACCTTCTT 1195

Qy       1470 TACTACCCCCAGACGCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGCTTCCTGCAG 1529
              || ||  ||          | |||  |  |||  |          |||  |    | | |
Db       1196 TATTATCCAAGAGTTAACCTGACCCGGTGCTCCAGCATCCCAGACATCATGGAACAGCTG 1255

Qy       1530 AAGTACTTCCACCTCATCAACAGGTTCA 1557
              ||| | ||  | | |   | |  | ||
Db       1256 CAGTTCATCGGCGTGAAGGAGATCTACA 1283


RESULT 38
HSDBH6
LOCUS       HSDBH6                    185 bp    DNA     linear   PRI 04-MAY-1990
DEFINITION  Human DNA for dopamine beta-hydroxylase exon 6 (EC 1.14.17.1).
ACCESSION   X13262
VERSION     X13262.1  GI:30467
KEYWORDS    alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 185)
  AUTHORS   Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
  TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
            different 3'-terminal regions are produced through alternative
            polyadenylation
  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 185)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
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  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES             Location/Qualifiers
     source          1. .185
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="9q34"
     intron          <1. .9
                     /note="Intron V (ca 3.4 kb)"
     mRNA            10. .176
                     /note="Exon 6"
     intron          177. .>185
                     /note="Intron VI (ca 3.5 kb)"
BASE COUNT       39 a     59 c     53 g     34 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.9e-21;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1013 AGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAA 1072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 AGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCCAAGCTGCGGCGCTTCAA 67

Qy       1073 CGCGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGA 1132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CGCGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTGATGGCCATTCCACCACGGGA 127

Qy       1133 GACCGCCTTCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGG 1182
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GACCGCCTTCATCCTCACTGGCTACTGCACGGACAAGTGCACCCAGCTGG 177


RESULT 39
AF129263/c
LOCUS       AF129263                2906 bp    mRNA    linear   PRI 22-JAN-2002
DEFINITION  Homo sapiens clone BPR-4 mRNA sequence.
ACCESSION   AF129263
VERSION     AF129263.1  GI:4928110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2906)
  AUTHORS   Gilbert,J.R., Kumar,A., Newey,S., Rao,N., Ioannou,P., Qiu,H.,
            Lin,D., Xu,P., Pettenati,M.J. and Pericak-Vance,M.A.
  TITLE     Physical and cDNA mapping in the DBH region of human chromosome
            9q34
  JOURNAL   Hum. Hered. 50 (3), 151-157 (2000)
  MEDLINE   20153491
   PUBMED   10686491
REFERENCE   2  (bases 1 to 2906)
  AUTHORS   Gilbert,J.R., Kumar,A., Newey,S. and Pericak-Vance,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1999) Center for Human Genetics, Duke University
            Medical Center, Research Park 2, DUMC, Durham, NC 27710, USA
FEATURES             Location/Qualifiers
     source          1. .2906
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9q34"
                     /clone="BPR-4"
                     /tissue_type="brain"
                     /note="maps to 152F5 cosmid in the Whitehead Inst. Ch 9
                     map; differentially processed version of clone BPR-5
                     sequence presented in GenBank Accession Number AF129264"
BASE COUNT      548 a    918 c    862 g    578 t
ORIGIN

  Query Match             6.1%;  Score 166.8;  DB 9;  Length 2906;
  Best Local Similarity   89.1%;  Pred. No. 4.9e-21;
  Matches  180;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       1512 GACGCCGGCTTCCTGCAGAAGTACTTCCACCTCATCAACAGGTTCAACAACGAGGATGTC 1571
             | | | ||| ||        |   ||||   ||  |  ||||||||||||||||||||
Db        463 GTCAGCTGCTCCCCAGCCTGGCTGTTCCTTGTCCCCGCCAGGTTCAACAACGAGGATGTC 404

Qy       1572 TGCACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTC 1631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TGCACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTTCACCTCTGTTCCCTGGAACTCCTTC 344

Qy       1632 AACCGCGACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAG 1691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 AACCGCGACGTACTGAAGGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAG 284

Qy       1692 TCCTCAGCCGTCCGCTTCCAGG 1713
             |||||||||||||||||||||||
Db        283 TCCTCAGCCGTCCGCTTCCAGG 262


RESULT 40
HSDBH11
LOCUS       HSDBH11                 178 bp    DNA     linear   PRI 04-MAY-1990
DEFINITION  Human DNA for dopamine beta-hydroxylase exon 11 (EC 1.14.17.1).
ACCESSION   X13267
VERSION     X13267.1  GI:30461
KEYWORDS    alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 178)
  AUTHORS   Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
  TITLE     Human dopamine beta-hydroxylase gene: two mRNA types having
            different 3'-terminal regions are produced through alternative
            polyadenylation
  JOURNAL   Nucleic Acids Res. 17 (3), 1089-1102 (1989)
  MEDLINE   89160241
   PUBMED   2922261
REFERENCE   2  (bases 1 to 178)
  AUTHORS   Nagatsu,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
            Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT     Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
FEATURES             Location/Qualifiers
     source          1. .178
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="9q34"
     intron          <1. .9
                     /note="Intron X (ca 0.6 kb)"
     mRNA            10. .169
                     /note="Exon 11"
     intron          170. .>178
                     /note="Intron XI (ca 0.9 kb)"
BASE COUNT       32 a     68 c     39 g     39 t
ORIGIN

  Query Match             6.0%;  Score 163.8;  DB 9;  Length 178;
  Best Local Similarity   98.8%;  Pred. No. 2.8e-20;
  Matches  165;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1547 CAACAGGTTCAACAACGAGGATGTCTGCACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTT 1606
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 CACCAGGTTCAACAACGAGGATGTCTGCACCTGCCCTCAGGCGTCCGTGTCTCAGCAGTT 63

Qy       1607 CACCTCTGTTCCCTGGAACTCCTTCAACCGCGACGTACTGAAGGCCCTGTACAGCTTCGC 1666
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         64 CACCTCTGTTCCCTGGAACTCCTTCAACTGCGACGTACTGAAGGCCCTGTACAGCTTCGC 123
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Qy       1667 GCCCATCTCCATGCACTGCAACAAGTCCTCAGCCGTCCGCTTCCAGG 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GCCCATCTCCATGCACTGCAACAAGTCCTCAGCCGTCCGCTTCCAGG 170
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